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Db 368 nstfrrvsvltvlnhgdvlnghdykckvsnkalpdpmqtkiskakgqprepyvyltppsr 427
QY 311 ELTRNOVSLTCLVKGFPSPDIAMWESNGOPENNKTTPVLDSDGSFFLYSKLTVDKSR 370
Db 428 eltkngvsltlcvkfyprrhlaewesngqpenyktctppldsdgsfflyskltvdksr 487
QY 371 WQGNVFSQSYMHALHNHYTQKSLSLSPG 400
Db 488 wqgnvfvscsvmhlaalnhytqkslslspg 517

RESULT 3
ID W60037 standard; Protein; 376 AA.
XX
AC W60037;
XX
DT 11-SEP-1998 (first entry)
XX
Antigenic peptide hFas (nd29) containing Fc region.
Fas ligand; Fas antagonist; apoptosis related disease; liver disease;
heart failure; kidney failure; graft-versus-host disease; antibody;
myocardial infarction; ischemic restenosis; endotoxic shock.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 1..16
FT /note= "hFas antigen signal peptide"
FT Protein 30..376
FT /note= "hFas (nd29) protein"

WC09818487-A1.
XX
PD 07-MAY-1998.
XX
PF 31-OCT-1997; 97WO-JP03978.
XX
PR 26-SEP-1997; 97JP-0262521.
PR 31-OCT-1996; 96JP-0290459.
PR 27-DEC-1996; 96JP-0351718.
XX
PA (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Suda T, Yatomi T;
WP1: 1998-271925/24.
N-PSDB; V34430.
XX
Use of Fas antagonist for treatment and prevention of
apoptosis-related diseases - such as heart or kidney failure,
graft-versus-host disease or liver disease
XX
Examples; Fig 5-9; 86pp; Japanese.
XX
This represents the antigenic peptide hFas (nd29) containing the Fc
region. The invention provides the use of Fas antagonist as an agent for
the treatment and prevention of apoptosis-related diseases. The Fas
antagonist can be a partial Fas antigen peptide containing the
extracellular part of the protein, but lacking the signal sequence, an
anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is
preferably a humanised antibody. The Fas antagonist is used in the
treatment and prevention of diseases such as myocardial infarction, heart
failure, ischemic heart disease, acute kidney failure, graft-versus-host
disease, ischemic restenosis of the heart, liver or kidney, and
endotoxic shock, and also as an organ preservative in transplantation.
The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
system.
XX
Sequence 376 AA;

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Query Match 60.4%; Score 1352; DB 19; Length 376;
Best Local Similarity 67.3%; Pred. No. 5; se-78;
Matches 270; Conservative 15; Mismatches 60; Indels 56; Gaps 9;

QY 8 LHYDETSHOLDKCPGTYLKHQCTAKM-KITVACACPD-HYITDSMHNDSDECTYCSPV 65
Db 23 lhhgqfchk---ppppgerkardctvngdepdcvpgqgkeytdkahlskrtcr-1 77
QY 66 CKELQYKOE--CNRTNHRVCECKEGRYLEIEFCLKHRSQCP---GFGVQACTPERRNT 119
Db 78 cdeghnglevleincrtitqntkrcrkpnfnfstvc---ehcdpckcehglikectlsnt 134
QY 120 VCKRCPDGFESNETSSAPCKRKTNCVFGLLTQKGNATHDNCISGNSSESTQKVDKTHT 179
Db 135 kcke--egszsnepks-----cdktht 154
QY 180 CPQCAPPELLGGPSVFLEFPPEKDTLMISRPEVTCVAVVDVSHEDPEKFMWYDGEVH 239
Db 155 cpqpapel199psvflfppxpkdtlmlstrpevtcvavvshedpevkfmwydvgevh 214
QY 240 NAKTRPEEQYNSTYRVVSVLTVLHODWLNKEXKCKVSNKALPAPLEKTSKAGQPRE 299
Db 215 naktkpreeqnystyrvvsvltvlnhgdvlnghdykckvsnkalpapelktskagqpre 274
QY 300 PQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMWESNGOPENNKTTPVLDSDGSFF 359
Db 275 pqvyltppsrdeltkngvsltlcvkfyprrhlaewesngqpenyktctppldsdgsff 334
QY 360 LYSKLTVDKSRWQGNVFSQSYMHALHNHYTQKSLSLSPG 400
Db 335 lyskltvdksrwqgnvfvscsvmhlaalnhytqkslslspg 375

RESULT 4
ID W50287 standard; Protein; 376 AA.
XX
AC W50287;
XX
DT 16-JUL-1998 (first entry)
XX
DE Human Fas antigen derivative/IgG1 Fc fusion.
XX
KW Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
apoptosis modulation; immunoglobulin G1 Fc; IgG1 Fc; fusion.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 1..16
FT Peptide /label= sig_peptide
FT Peptide 17..376
FT /label= mat_peptide

WC09742319-A1.
XX
PD 13-NOV-1997.
XX
PF 01-MAY-1997; 97WO-JP01502.
XX
PR 02-MAY-1996; 96JP-0135760.
XX
PA (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N;
WP1: 1997-558981/51.
N-PSDB; V07004.
XX

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PR Fas antigen derivative containing modified extracellular region -
 PR has low antigenicity, promotes apoptosis and is useful in treatment
 of viral and other diseases

PS Disclosure: Fig 4; 102pp; Japanese.

CC The present sequence is a Fas antigen derivative/IgG1 Fc
 CC fusion, which contains a Fas antigen extracellular region lacking
 CC one or more amino acid residues in the region from the
 CC amino-terminal to (but excluding) the 1st cysteine residue
 CC (preferably at least 29 residues are deleted).

CC The derivative is an effective regulator of apoptosis and can be
 CC used (either by administration of the polypeptide, or by the use
 CC of the coding DNA in gene therapy) to treat a range of diseases,
 CC e.g. diabetes, arthritis, lupus and in particular viral diseases
 CC such as hepatitis, influenza and HIV, by modulating apoptosis of
 CC virus-infected cells.

Sequence 376 AA;

Query Match 59.7%; Score 1337; DB 18; Length 376;
 Best Local Similarity 66.6%; Pred. No. 4,8e-77;
 Matches 267; Conservative 16; Mismatches 62; Indels 56; Gaps 9;

QY 8 LHYDETSHOLLCDKCPPTLYLKOHCTAKW-KTVCAPCPD-HYTPDSWTSDECLYCSFV 65

DB 23 lhdqgfcfk-----pcpgerkarcdetvngdpcdvpcqegkyektdkafskrrcr-1 77

QY 66 CKELOYVKE--CNRTNHNVCSECKEGRYLEIEFCLNHRSCP---GFGVQAGTPERNY 119

DB 78 cdegnglevelnctrqntkrcrkpfncnstvc---ehcdpckcchnglikectltnt 134

QY 120 VKKRCRDFEFNSHTSKACRKHTNCSVGLLLTOKGNATHDNICGNSBSQKVDKHTT 179

DB 135 kcke--egrsneps-----cckltnt 154

QY 180 CFPAPAPELLGSPVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVFNMYVDGEVH 239

DB 155 cpcpapelsgpsvflfprkpxdtlmisrptevtcvvvdshedevfnmyvdgvevh 214

QY 240 NAKTRPREQYNSTYRVSVLTVLHODMNGKEYKCKVSNKALPADIETISKAKQPRE 299

DB 215 naktkpreeqynstyrvsvltvlhqdwnlqgkyckvsnkalpadietiskakqpre 274

QY 300 PQRVTLPRSDLTKNQVSLTCLVKGFPDIAVWESNGQENNYKTPRVLDSPGSF 359

DB 275 pqrvtlprsdeltknqvsltclvkgfypsdlavewesngqpnnyktprvldsgsf 334

QY 360 IYSKLTVDKSRMQGVNFCQSVNHEALHNHYOKSLSPG 400

DB 335 lysnltvdksrvgqgnvfscsymhealhnhytqkslspg 375

RESULT 5

ID R81882 standard; Protein; 438 AA.

AC R81882;

DT 30-MAR-1996 (first entry)

DE Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.

XX OX40; OX40-L; cytokine; cell surface molecule; plasmid;

KW pDC406/OX40/Fc*; membrane glycoprotein.

XX Synthetic.

XX US5457035-A.

XX 10-OCT-1995.

XX PD

PF 23-JUL-1993; 93US-0097827.

XX 23-JUL-1993; 93US-0097827.

XX (IMMUNEX CORP.

PA Baum PR, Fanslow WC, Gayle RB, Goodwin RG;

PI WPT. 1995-357992/46.

DR N-PSDB; T00829.

XX New isolated DNA encoding the OX40 ligand polypeptide - also vectors

PR and host cells, used to produce recombinant ligand used in e.g.

CC prim. T cell culture, to modulate immune response etc.

CC Example 2; Column 35-38; 26pp; English.

PS This plasmid encodes an OX40/Fc antibody fragment mutein protein,

CC and is used to express a soluble OX40/Fc mutein fusion protein for

CC use in detecting cDNA clones encoding a OX40 ligand. The Fc

CC fragment may be derived from human IgG1, and the plasmid may be

CC used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell

CC line. Culture supernatant was purified by affinity chromatography

CC and this was used, together with labeled goat anti-human IgG to

CC screen various cell lines.

Sequence 438 AA;

Query Match 59.5%; Score 1332; DB 16; Length 438;

Best Local Similarity 62.4%; Pred. No. 1.2e-76;

Matches 262; Conservative 23; Mismatches 75; Indels 60; Gaps 6;

QY 20 CDKCPRTYLYKOHCTAKW-KTVCAPCPD-HYTPDSWTSDECLYCSFV 77

DB 39 cdegnglevelnctrqntkrcrkpfncnstvc---ehcdpckcchnglikectltnt 96

QY 78 RTHNHNVCSECKEGRYLEIEFCLNHRSCP---GFGVQAGTPERNY 137

DB 97 pldqgfcfk-----cckltnt 154

QY 138 PCKRHTNCSVGLLLTOKGNATHDNICGNSBSQKVDKHTT 179

DB 138 ackpntnctlsqkqtrhpasdelavcedrsllatllwetqprftprvtgsltwprts 197

QY 172 -----QKVNKTPRSDLTKNQVSLTCLVKGFPDIAVWESNGQENNYKTPRVLDSPGSF 220

DB 198 elpstrplvrscckltncpcpaeagarsvflfprkpxdtlmisrptevtcvvvdshedevfnmyvdgvevh 257

QY 221 SHEDPEVFNMYVDGEVHNAKTRPREQYNSTYRVSVLTVLHODMNGKEYKCKVSNK 280

DB 258 shedpevfnmyvdgvevhnaaktkpreeqynstyrvsvltvlhqdwnlqgkyckvsnk 317

QY 281 ALPADIETISKAKQPREPOVYTLPRSDLTKNQVSLTCLVKGFPDIAVWESNGQ 340

DB 318 alpadietiskakqprepqytlprsdeltknqvsltclvkgfypsdlavewesngq 377

QY 341 PENNYKTPRVLDSPGSFVLSKLTVDKSRMQGVNFCQSVNHEALHNHYOKSLSPG 400

DB 378 pennyktprvldsgsfvlskltvdksrvgqgnvfscsymhealhnhytqkslspg 437

RESULT 6

ID W48976 standard; Protein; 438 AA.

AC W48976;

DT 25-SEP-1998 (first entry)

DE OX40/Fc mutein.

XX OX40; OX40-L; cytokine; T cell antigen; TH-2 immune response; OX40-L;

KW


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KM chimeric.
XX Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
XX Key Location/Qualifiers
FH Region 1..206 "Extracellular domain of mouse OX40"
FT /note="Extracellular domain of mouse OX40"
FT Region 207..438
FT /note="Mutant Fc region of human IgG1 antibody"
FT Misc-difference 225
FT /note="Changed from Leu in wild-type to Ala in mutant"
FT Misc-difference 226
FT /note="Changed from Leu in wild-type to Gly in mutant"
FT Misc-difference 228
FT /note="Changed from Gly in wild-type to Ala in mutant"
XX
XX US5783665-A.
PD 21-JUL-1998.
XX
XX 22-JUN-1995; 95US-0494574.
XX
XX 23-JUL-1993; 93US-0097827.
XX
XX 22-JUN-1995; 95US-0494574.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX WPI; 1998-427099/36.
XX
XX N-PSDB; V32636.
XX
XX Purified polypeptide OX-40 ligands - for co-stimulation of T-cell
XX production and binding assays for OX-40 and homologues
XX
XX Example 2; Col 37-40; 26pp; English.
XX
XX The present sequence represents the OX40/Fc fusion protein that
XX contains the extracellular domain of mouse OX40 fused to the mutated
XX Fc region of the human IgG1 antibody. The fusion protein was used
XX for detecting cDNA clones encoding an OX40 ligand. The invention
XX claims for a murine OX40-L cytokine (M48975) that binds to the murine
XX T cell antigen, OX40. The OX40-L protein is claimed to be useful for
XX co-stimulation of T-cell production and in binding assays for
XX detecting OX40 or its homologues. The OX40-L protein is also claimed
XX to generate a TH-2 immune response.
XX
SQ Sequence 438 AA:
XX
Query Match 59.5%; Score 1332; DB 19; Length 438;
Best Local Similarity 62.4%; Pred. No. 1.2e-76;
Matches 26; Conservative 23; Mismatches 75; Indels 60; Gaps 6;
XX
XX 20 CDKCPGTYLKONCTARKWTCAPCPDHYTD--SWHTSDCLYCSFYCKELQYKOCN 77
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 39 crecpghgmwnrdhtrdichpcetgfyneavnydctckqctcgnh--rsgselknc 96
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 78 RTHNRVCEKGRLEIEFLCKHRSCTPPGFCVVOAGTPERTVTKRCPDGFSTETSKA 137
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 97 ptgtvtvrcr-----pjtpirgdsyglqvdvcppepghfs--pqnq 137
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 138 PCRHTKSNVFGLLTQGNATHNICSNS-----EST----- 171
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 138 ackwtcttsgktrhpasclavcedrsllattlwtcgrptftrvtvsttwpts 197
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 172 -----QKVDKTHTCPPCPAPELLGSPVFLPPPKFKDITMISRPPEVTCVVVDV 220
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX 198 elptptlvprsdckhtcpcpapaegagsvflfpkpkcdlmlstrfpevcvavdv 257

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OY 221 SHEDEPTEFNMYVDGVVHNAKTKPREEOYNSTRVSVLTVLHODPLNGEKYCKYSNK 280
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 258 shedpewkfmydygvvhnaktkpreeynstyrsvsvltvlhgdwlngkeyckysnk 317
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 281 ALPAPIKTSKAKGQPREPOVYTLPPSRDELFTKNQVSLCIVKGFPSDIAVWESNGQ 340
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 318 alpapekttskagqgprepqvylppsrdeitknqyslclvkgfypsdlavwesngq 377
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 341 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRMOOGNVFSCSVMEALNNHYTOKSLSPG 400
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 378 pennykttppvldsdgsfflyskltvdkstrwqgnvscsvmealnnhytqslslspg 437
XX |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
XX
XX RESULT 7
XX ID Y68949 standard; Protein; 764 AA.
XX
XX AC Y68949;
XX
XX 30-MAY-2000 (first entry)
XX
XX DE Fusion protein of murine delta-related protein and human IgG Fc.
XX
XX KW Cell development cycle; Delta family; membrane surface-bound ligand;
XX endothelial cell biology; gene therapy; subcortical infarct;
XX KW cerebral autosomal dominant ateliopathy; leucoencephalopathy;
XX ischaemic stroke; chimera.
XX
XX OS Chimeric - Mus sp.
XX
XX OS Chimeric - Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT 1..529
XX FT /note="Extracellular region of the murine
XX FT delta-related protein"
XX FT Protein 533..764
XX FT /note="human IgG Fc portion"
XX
XX PN WO200006726-A2.
XX
XX PD 10-FEB-2000.
XX
XX PF 12-JUL-1999; 99WO-US15710.
XX
XX PR 27-JUL-1998; 98US-0123168.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Shutter JR, Stark KL;
XX
XX WPI; 2000-195294/17.
XX
XX DR N-PSDB; Z60536.
XX
XX Cell development cycle protein of delta family useful for treating
XX various disorders associated with central nervous system e.g. cerebral
XX autosomal dominant ateliopathy and ischemic strokes
XX
XX Example 6; Page 169-171; 171pp; English.
XX
XX The present sequence represents a fusion protein of the extracellular
XX domain of a murine polypeptide, which a member of the cell
XX development cycle protein family known as the Delta family of
XX mammalian membrane surface-bound ligands, and the human immunoglobulin
XX G (IgG) Fc portion. The murine delta-related protein gene is expressed
XX within vascular endothelium indicates a role for the polypeptides
XX in the control of endothelial cell biology. The murine polynucleotide
XX was identified from a white adipose tissue cDNA library. The polypeptide
XX is useful for identifying receptors, which bind to and/or are activated
XX by the polypeptide. The polynucleotide is useful in gene therapy of
XX cerebral autosomal dominant ateliopathy with subcortical infarcts and
XX leucoencephalopathy, an autosomal dominant disorder causing ischemic
XX strokes.

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514 IUSUGSISITYSALCVDAKASITWGGUUVLSICSVMUUEAMUNNYCQHSISISPY 502

glomerulonephritis, proliferative vitreoretinopathy, myelofibrosis;
 collagen vascular disease, e.g. systemic sclerosis, polymyositis,
 scleroderma, dermatomyositis or systemic lupus erythematosus; and
 fibrosis associated with stenosis. It is also useful for treating
 wounds, to prevent overproduction of connective tissue and so prevent
 adhesions or scarring, and to prevent post-radiation fibrosis (by
 administration to patients about to undergo radiation therapy).

Sequence 388 AA;

Query Match 55.9%; Score 1252.5; DB 21; Length 388;

Best Local Similarity 65.7%; Pred. No. 1e-71; Mismatches 70; Indels 47; Gaps 10;

Matches 257; Conservative 17; Mismatches 70; Indels 47; Gaps 10;

37 WKTYCAPCPDHY-----TDSWHTSDE-----CLYC--SPVCKELQYKQECNRTHN 81
 17 wtlastiprhvqkvsndmvdnngavkfprqckfcdrstcdnqkscmsncstl-- 74
 82 RVCECKEGRYLIEFCLKHRCSPGFGVVOAGTPERNVCKRCPD-----GFSNERTSS 135
 75 sice-----kahevcv---awrkndentletvchdpklayhflledsas 118
 136 KAPCRKHTNCSVFG---LLTQKGNATHDNICSGNSESTOK---VDKTHTCPCPAPRL 189
 119 pkclmkek--kvfgctfmcscstdecndhlfseeytsspdvdkthtccppapell 176
 190 GGSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMYDGVENNAKTRPREQ 249
 177 gpgvflfpkpkdtlmisrtpevtcvvdvshdpevkfmydgvvhnaktrpreeq 236
 250 YNSTYRVAVSVTLVHOMLNKEKVKCNKALPAPITKTSKAGOREPOVYTLIPSR 309
 237 ynstyrvavsvtlvhdqngkeykckvsnkalpalektlskagqpreqvylipstr 296
 310 DELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPVLDSGSEFLYSLKLVYDKS 369
 297 deltkngvslclvkgfypsdiavemesngopennyktptpvlsgsflyskltvdk 356
 370 RMOGQNVFSCSVHHEALHNHTOKSLSPG 400
 357 rwgqgnvfscsvhhealhnhtqkslspg 387

RESULT 11

W71603 standard; Protein; 664 AA.

W71603;

19-NOV-1998 (first entry)

Human neuturin receptor alpha/Fc sequence (IFP2a) fusion protein.

Human neuturin receptor alpha; NTN-1alpha; variant; chimeric;

Human protein; immunoadhesion; ret-expressing cell; neurological;

renal; haematological disease.

Synthetic.

Homo sapiens.

MO9836072-A1.

20-AUG-1998.

17-FEB-1998; 98MO-USO3179.

24-OCT-1997; 97US-0957063.

16-FEB-1997; 97US-0802805.

09-JUN-1997; 97US-0871913.

(GETH) GENENTECH INC.

PI Hynes MA, Klein RD, Rosenthal A;

XX WPI; 1998-467175/40.

DR N-PSDB; V58006.

XX New polypeptide(s) based on human neuturin receptor alpha and

PT related nucleic acid - useful for increasing survival of

PT ret-expressing cells for treating e.g. neurological, renal and

PT haematological diseases

PS Example 3; Page 81-83; 116pp; English.

XX The present sequence represents human neuturin receptor alpha
 CC (NTN-1alpha)/Fc sequence (IFP2a) fusion protein, from an example of the
 CC present invention. NTN-1alpha proteins can be used: (a) to identify
 CC molecules that bind specifically to it (potential agonists and
 CC antagonists) and to purify such compounds; (b) to modulate response of
 CC cells to neuturin (NTN); (c) to increase survival of Ret-expressing
 CC cells or to activate Ret on the surface of cells (soluble glial derived
 CC neurotrophic factor receptor (GDNF alpha) may be used the same way);
 CC (d) to increase the half-life of cognate ligands (especially NTN); (e)
 CC diagnostically to determine serum levels of its ligands; and (f) as
 CC animal feed additive or molecular weight marker. NTN-1alpha, its genes,
 CC (ant)agonists and antisense nucleic acids, are useful in vivo or ex vivo
 CC for treating conditions related to abnormal NTN activity or response,
 CC particularly neurological (central or enteric), renal or haematopoietic
 CC (spleen) diseases or injuries. Ab may be agonists or antagonists for
 CC therapeutic use (e.g. as antagonists to treat excessive/unwanted NTN-
 CC alpha expression, e.g. in some tumours), also reagents for immunoassay
 CC and affinity purification.

SO Sequence 664 AA;

Query Match 55.8%; Score 1249.5; DB 19; Length 664;

Best Local Similarity 63.6%; Pred. No. 3e-71; Mismatches 264; Conservative 23; Mismatches 57; Indels 71; Gaps 14;

32 HCTAKMKTGACPC-DHY-----YDSWHTSDECLYCSPVCKELQY 72
 274 ncrasyqltvs-cpadnqgacslsyagmifdmtpnvdsptg---lvvspc----- 323
 73 KOECNRTHNHNVECKEGRYLIEF---CLKH-----RSCP--PGFGVVOAGTP 115
 324 --scrsgsmeeeee--kflr-dftenpolnmalqatngtdvnpakgsgfatqgprv 378
 116 ERNTVCKRCPDGFPSNFTSSKAPCRKHTNCSVFGLLITQKGNATHD-----NICS 165
 379 ekt--psloddslsdslstslgtsvltctsvgeglj---kanskelsmcftelttlp 431
 166 GNSSEIQVYDKTHNCPCPAPRLLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDP 225
 432 gprid--pvckthtchpcpapelldgsvflfpkpkdtlmisrtpevtcvvdvshedp 488
 226 EVKENWYVDGVENNAKTRPREQYNSTYRVAVSVTLVHOMLNKEKVKCNKALPAP 285
 489 evkfnwyvdgvvhnaktrpreeqynstlyrvavsvtlvhdqngkeykckvsnkalpap 548
 286 IEKTSKAKGQPREPOVYTLIPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNY 345
 549 iektlskagqprepyytlipsrdeemtknvaltclvkgfypsdiavemesngopenny 608
 346 KTPPVLDSDGSEFLYSLKLVYDKSRMOGQNVFSCSVHHEALHNHTOKSLSPG 400
 609 ktpplvdsgsflyskltvdksrwqgnvfscsvhhealhnhtqkslspg 663

RESULT 12

Y80123 standard; Protein; 664 AA.

Y80123;

Y80123;

QY 201 PKDTLMISRTPEVTCVYVDSHEDEPEVKENMYVDGVEVHNNAKTKPREBOYNSTYRVSVL 260
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CC 245 PKDTLMISRTPEVTCVYVDSHEDEPEVKENMYVDGVEVHNNAKTKPREBOYNSTYRVSVL 304
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 261 TVLHODWLNKREYKCKVSNKALPAPIEKTISKAKGPREPOVYTLPSRDELTKNQVSLT 320
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 305 tvlhqdwlngreykckvsnkalpapiektiskakgqprepyytlpsrdeltknqvalt 364
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 321 CLVKGFTYSDDAVEMESNGOPENNKITPPVLDSDGSFFLYSKLTVDSKRMQGNVFCSS 380
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 365 clvkgftysddavemessngopennyktlppvldsdgsfflyskltvdksrwmqgnvfscs 424
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 381 VMHEALHNHYTKOKSLSPG 400
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 425 vmhealhnhytkokslslspg 444
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 14
 W71604 standard; Protein; 664 AA.
 AC W71604;
 DT 19-NOV-1998 (first entry)
 XX
 DE Rat neuritin receptor alpha/Fc sequence (IIF2a) fusion protein.
 XX
 KW Human; neuritin receptor alpha; NTNR-alpha; variant; chimeric;
 KW fusion protein; immunoadhesion; ret-expressing cell; neurological;
 KW renal; haematological disease.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS Rattus sp.
 XX
 PN MO9836072-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 17-FEB-1998; 98WO-US03179.
 XX
 PR 24-OCT-1997; 97US-0957063.
 PR 18-FEB-1997; 97US-0802805.
 PR 09-JUN-1997; 97US-0871913.
 XX
 PA (GETH) GENENTECH INC.
 Hynes MA, Klein RD, Rosenthal A;
 WPI: 1998-467175/40.
 DR N-PSDB: V58007.
 PT New polypeptide(s) based on human neuritin receptor alpha and
 PT related nucleic acid - useful for increasing survival of
 PT ret-expressing cells for treating e.g. neurological, renal and
 PT haematological diseases
 XX
 PS Example 3; Page 84-86; 116pp; English.
 CC
 CC The present sequence represents rat neuritin receptor alpha
 CC (NTNR-alpha)/Fc sequence (IIF2a) fusion protein, from an example of the
 CC present invention. NTNR-alpha proteins can be used: (a) to identify
 CC molecules that bind specifically to it (potential agonists and
 CC antagonists) and to purify such compounds; (b) to modulate response of
 CC cells to neuritin (NTN); (c) to increase survival of Ret-expressing
 CC cells or to activate Ret on the surface of cells (soluble glial derived
 CC neurotrophic factor receptor (GDNFR alpha) may be used the same way);
 CC (d) to increase the half-life of cognate ligands (especially NTN); (e)
 CC diagnostically to determine serum levels of its ligands; and (f) as
 CC animal feed additive or molecular weight marker. NTNR-alpha, its genes,
 CC (ant)agonists and antisense nucleic acids, are useful in vivo or ex vivo
 CC for treating conditions related to abnormal NTN activity or response,
 CC particularly neurological (central or enteric), renal or haematopoietic

CC (spleen) diseases or injuries. Ab may be agonists or antagonists for
 CC therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-
 CC alpha expression, e.g. in some tumours), also reagents for immunoassay
 CC and affinity purification.
 XX
 SO Sequence 664 AA;
 Query Match 55.7%; Score 1248.5; DB 19; Length 664;
 Best Local Similarity 62.7%; Pred. No. 3,4e-71;
 Matches 261; Conservative 21; Mismatches 61; Indels 73; Gaps 11;
 QY 32 HCTAKMKTVCAPCP-DHY-----YTDSWHTSDECLYCSPVCKELQYV 72
 Db 274 ncrasylrits-cpadnygaalgsyagmifdmtprnydsnptp---lvspwc----- 323
 QY 73 KOECNRHNRVCEKE-----GRLEIEFCLKHNSCPGEGVQAGT 114
 Db 324 --ncrgsgmneeceklfrdftempclrnaiaqafngtdvmmpskpplp---atqapr 377
 QY 115 PERNTVCKRCPDGFFSNSTSSKAPCRKHTNGSVFGLLTOKGNATHD-----NIC 164
 Db 378 vekt---pslpddlsdstslgtsvltctstsqegll---kanskelsmfteltnls 430
 QY 165 SGNSESTQKVDKTHTCPPCAPPELLGSPSVLFPPPKRDTLMISRTPEVTCVYVDSHED 224
 Db 431 pg---srdpvkhtntpcpcpapel1lgpsvflfppkxdtlmisrtpevtcvvvdshed 487
 QY 225 PEVKFMYVDGVEVHNNAKTKPREBOYNSTYRVSVLTVLHODWLNKREYKCKVSNKALPA 284
 Db 488 pevxfmyvdgvevhnaktkpreegynstyrvsvlvtlhqdwlngreykckvsnkalpa 547
 QY 285 PIEKTISKAKGPREPOVYTLPSRDELTKNQVSLTCLVKGFTYSDDAVEMESNGOPENN 344
 Db 548 piektiskakgprepyytlpsrdeemtknqvaltclvkgftysddavemessngopenn 607
 QY 345 YKTPPVLDSDGSFFLYSKLTVDSKRMQGNVFCSSVMHEALHNHYTKOKSLSPG 400
 Db 608 yktppvldsdgsfflyskltvdksrwmqgnvfscsvmhealhnhytkokslslspg 663
 RESULT 15
 Y80124 standard; Protein; 664 AA.
 ID Y80124
 AC Y80124;
 DT 19-MAY-2000 (first entry)
 XX
 DE Rat NTNR alpha and Igg fusion protein SEQ ID NO:18.
 XX
 KW Human; neuritin receptor alpha; NTNR alpha; splenic haematopoiesis;
 KW anaemia; Chromocytopenia; hypoplasia; haemorrhage.
 XX
 OS Rattus sp.
 OS Synthetic.
 XX
 PN US6025157-A.
 XX
 PD 15-FEB-2000.
 XX
 PF 24-OCT-1997; 97US-0957063.
 XX
 PR 18-FEB-1997; 97US-0038839.
 PR 09-JUN-1997; 97US-0049818.
 XX
 PA (GETH) GENENTECH INC.
 Hynes MA, Rosenthal A, Klein RD;
 WPI: 2000-181808/16.
 DR N-PSDB: 291460.
 XX

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2000, 10:53:53 ; Search time 27.53 Seconds
(without alignments)
243.533 Million cell updates/sec

Title: US-09-389-545-5

Perfect score: 2240

Sequence: 1 EITFPKYLHDETSQQLC.....VMHEALHNYTKSLSPG 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

1 number of hits satisfying chosen parameters: 164575

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 1510.5 | 67.4 | 486 | 1 | US-08-243-010-1 |
| 2 | 1502 | 67.1 | 518 | 1 | US-08-385-229-4 |
| 3 | 1332 | 59.5 | 438 | 1 | US-08-097-827-11 |
| 4 | 1332 | 59.5 | 438 | 1 | US-08-494-574-11 |
| 5 | 1266.5 | 56.5 | 911 | 2 | US-08-484-438-10 |
| 6 | 1249.5 | 55.8 | 664 | 3 | US-08-957-063-16 |
| 7 | 1248.5 | 55.7 | 664 | 3 | US-08-957-063-18 |
| 8 | 1243.5 | 55.5 | 449 | 3 | US-08-897-236-23 |
| 9 | 1240.5 | 55.4 | 387 | 1 | US-08-470-299-4 |
| 10 | 1238.5 | 55.3 | 442 | 4 | PCT-US96-10043-9 |
| 11 | 1238 | 55.3 | 396 | 2 | US-08-784-512-3 |
| 12 | 1237 | 55.2 | 347 | 1 | US-07-940-861-43 |
| 13 | 1237 | 55.2 | 347 | 1 | US-08-459-512-43 |
| 14 | 1237 | 55.2 | 347 | 2 | US-08-459-657-43 |
| 15 | 1237 | 55.2 | 347 | 2 | US-08-460-132-43 |
| 16 | 1237 | 55.2 | 347 | 4 | PCT-US92-02050-43 |
| 17 | 1234 | 55.1 | 371 | 1 | US-08-236-311-7 |
| 18 | 1234 | 55.1 | 371 | 1 | US-08-457-918-7 |
| 19 | 1234 | 55.1 | 449 | 1 | US-08-458-516-13 |
| 20 | 1234 | 55.1 | 459 | 1 | US-08-157-101A-7 |
| 21 | 1234 | 55.1 | 476 | 2 | US-08-378-939-10 |
| 22 | 1234 | 55.1 | 476 | 3 | US-08-487-550-4 |
| 23 | 1234 | 55.1 | 476 | 3 | US-08-487-550-12 |
| 24 | 1234 | 55.1 | 478 | 3 | US-08-487-550-8 |
| 25 | 1228 | 54.8 | 232 | 2 | US-08-593-043A-50 |
| 26 | 1228 | 54.8 | 254 | 2 | US-08-284-391B-33 |
| 27 | 1228 | 54.8 | 424 | 4 | PCT-US95-03866-12 |
| 28 | 1228 | 54.8 | 424 | 4 | PCT-US95-03866-14 |

| | | | | | | |
|----|--------|------|-----|---|-------------------|-------------------|
| 29 | 1228 | 54.8 | 437 | 4 | PCT-US96-10043-11 | Sequence 11, Appl |
| 30 | 1228 | 54.8 | 451 | 2 | US-08-887-352B-14 | Sequence 14, Appl |
| 31 | 1228 | 54.8 | 451 | 2 | US-08-887-352B-16 | Sequence 16, Appl |
| 32 | 1228 | 54.8 | 451 | 2 | US-08-887-352B-18 | Sequence 18, Appl |
| 33 | 1228 | 54.8 | 451 | 3 | US-08-466-151-65 | Sequence 65, Appl |
| 34 | 1228 | 54.8 | 452 | 3 | US-09-027-449-71 | Sequence 71, Appl |
| 35 | 1228 | 54.8 | 453 | 3 | US-08-466-151-8 | Sequence 8, Appl |
| 36 | 1228 | 54.8 | 454 | 2 | US-07-934-373C-22 | Sequence 22, Appl |
| 37 | 1228 | 54.8 | 454 | 2 | US-08-437-642B-22 | Sequence 22, Appl |
| 38 | 1228 | 54.8 | 454 | 4 | PCT-US93-07832-22 | Sequence 22, Appl |
| 39 | 1226.5 | 54.8 | 442 | 1 | US-08-461-968A-5 | Sequence 5, Appl |
| 40 | 1226.5 | 54.8 | 442 | 2 | US-08-462-571-5 | Sequence 5, Appl |
| 41 | 1217.5 | 54.4 | 552 | 1 | US-08-243-010-6 | Sequence 6, Appl |
| 42 | 1207 | 53.9 | 232 | 1 | US-07-797-556-4 | Sequence 4, Appl |
| 43 | 1207 | 53.9 | 232 | 1 | US-08-225-889-4 | Sequence 4, Appl |
| 44 | 1207 | 53.9 | 232 | 1 | US-08-570-923-4 | Sequence 4, Appl |
| 45 | 1207 | 53.9 | 232 | 4 | PCT-US95-06530-4 | Sequence 4, Appl |

ALIGNMENTS

RESULT 1
US-08-243-010-1
Sequence 1, Application US/08243010
Patent No. 5639597
GENERAL INFORMATION:
APPLICANT: Lafuier, Leander
APPLICANT: Zettlmeissel, Gerd
APPLICANT: Oquendo, Patricia
TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,010
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1132-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 486 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-243-010-1
Query Match 67.4%; Score 1510.5; NB 1; Length 486;
Best Local Similarity 65.2%; Pred. No. 1.6e-118;

Matches 292: Conservative 17: Mismatches 76: Indels 63: Gaps 5:

```

OY 9 HYDEETSHQLLDCKPPGYTLKQHCIAKKTVCAPCPDHYTDSMTSDECLYCSVPCKE 68
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 45 YYDQ--TAQMCSSKSPGGHAKVFCRTSDTVCDSCEDSTYTQLMNWMVBECLSCGSCSS 102
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 69 LQYVKECNRTHNRVCEKEGRYLEI-----EFLKHSRCPGFGVVOAGTPERNYVCK 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 103 DQVETQACTREONRITCTCRPGWYCALSKQEGCRLCAPLKRCPGFGVARGTETSDYVCK 162
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 123 RCPDGFESNETSSKAPCRKRTNCSVFGLLLTQGNATHDNICSGNS----- 168
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 163 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 218
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 169 -----ESTQKVDKHTCPCPAPPELLGGP 192
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 PVSTRSQHTQTPPEPSTABSTFLLPMGSPPAEGSTGDEPKSCDKHTHCPCPAPPELLGG 278
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 193 SVFLPPKPKDITLMISTRTPEVTCVVDVSHEDPEVKFNMTYVDGEVHNATKPREDOYNS 252
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 279 SVFLPPKPKDITLMISTRTPEVTCVVDVSHEDPEVKFNMTYVDGEVHNATKPREDOYNS 338
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 253 TYRVSVLTLYLHODWLNKGEYKCKVSNKALPAPIEKTISAKQOPREPOVYTLPPSRDEL 312
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 339 TYRVSVLTLYLHODWLNKGEYKCKVSNKALPAPIEKTISAKQOPREPOVYTLPPSRDEL 397
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 313 TKNOVSLTCLVKGFFPSDIAVEMESNGQPPNNYKTPPVLDSDGSFFLYSKLTVDKSRM 372
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 398 TKNOVSLTCLVKGFFPSDIAVEMESNGQPPNNYKTPPVLDSDGSFFLYSKLTVDKSRM 457
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 373 QGNVFCSCVMEALHNHYTOKSLSLSPG 400
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 458 QGNVFCSCVMEALHNHYTOKSLSLSPG 485
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 2
US-08-385-229-4
Sequence 4, Application US/08385229
Patent No. 5605690
GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,229
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 518 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-385-229-4

Query Match 67.1%; Score 1502; DB 1; Length 518;
Best Local Similarity 63.8%; Pred. No. 8,9e-118;
Matches 287: Conservative 21: Mismatches 78: Indels 64: Gaps 4:

```

OY 9 HYDEETSHQLLDCKPPGYTLKQHCIAKKTVCAPCPDHYTDSMTSDECLYCSVPCKE 68
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 YYDQ--TAQMCSSKSPGGHAKVFCRTSDTVCDSCEDSTYTQLMNWMVBECLSCGSCSS 131
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 69 LQYVKECNRTHNRVCEKEGRYLEI-----EFLKHSRCPGFGVVOAGTPERNYVCK 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 DQVETQACTREONRITCTCRPGWYCALSKQEGCRLCAPLKRCPGFGVARGTETSDYVCK 191
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 123 RCPDGFESNETSSKAPCRKRTNCSVFGLLLTQGNATHDNICSGNS----- 168
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 169 -----ESTQKVDKHTCPCPAPPELLG 190
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 PVSTRSQHTQTPPEPSTABSTFLLPMGSPPAEGSTGDEPKSCDKHTHCPCPAPPELLG 307
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 191 GRSVFLPPKPKDITLMISTRTPEVTCVVDVSHEDPEVKFNMTYVDGEVHNATKPREDOY 250
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 GRSVFLPPKPKDITLMISTRTPEVTCVVDVSHEDPEVKFNMTYVDGEVHNATKPREDOY 367
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 251 NSTYRVSVLTLYLHODWLNKGEYKCKVSNKALPAPIEKTISAKQOPREPOVYTLPPSRD 310
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 NSTYRVSVLTLYLHODWLNKGEYKCKVSNKALPAPIEKTISAKQOPREPOVYTLPPSRD 427
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 311 ELTKNOVSLTCLVKGFFPSDIAVEMESNGQPPNNYKTPPVLDSDGSFFLYSKLTVDKSR 370
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 428 ELTKNOVSLTCLVKGFFPSDIAVEMESNGQPPNNYKTPPVLDSDGSFFLYSKLTVDKSR 487
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 371 WOQNVFCSCVMEALHNHYTOKSLSLSPG 400
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 488 WOQNVFCSCVMEALHNHYTOKSLSLSPG 517
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 3
US-08-097-827-11
Sequence 11, Application US/08097827
Patent No. 5457035
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Ranslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el cytokine which is a ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

```

? NAME: Perkins, Patricia A.
? REGISTRATION NUMBER: 34,693
? REFERENCE/DOCKET NUMBER: 2800
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 206-587-0730
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 438 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
?
? US-08-057-827-11

```

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 59.5% | Score 1333; | DB 1; | Length 438; |
| Best Local Similarity | 62.4%; | Pred No. 1.1e-103; | | |
| Matches 252; | Conservative 23; | Mismatches 75; | Indels 60; | Gaps 6 |

```

QY      20  CDKCPRGYLLKONHCAKMTKATKATYACAPRDHYND--SMHSDCLCSRYKCLQYQJECN  77
      39  CREOCPGKGMVNRCDHTDITLCHPCETGFYMEANVNYDCKCKTQCNH--BGSGLKONCT  96
      78  RTHNRCVCECKEGRYLLEIFCLKHRSKCPGFCGVQAGPERNTYVCKRCPDGEFFNETSKA  137
Db      97  PTDYVCCR-----PGTPRODSGYKLGVDVCPCPGHFS--PGNNQ  133
QY      138  PCRKHTNCSVGGLLLTQKGNATHDNICGNS-----EST-----  171
Db      138  ACKPWTNCTLSGKOTRHPASDSLAVCEDRSLATLMTETORPTFRPTVOSTVWPTS  197
QY      172  -----QKDKTHTCPPCAPBELDGSVFLPPRKCDLMTSRPEYVCVVVD  228
Db      198  ELPSTPIVBERSCDQHTTCCPPCPAREGASVFLPFRKCDLMTSRPEYVCVVVD  257
QY      221  SHEDPEYVFNMYVDGEVHNNAKTRPREQOYSTRVVSVLEVLQDMVNGREYCKCKYSNK  280
Db      258  SHEDPEYVFNMYVDGEVHNNAKTRPREQOYSTRVVSVLEVLQDMVNGREYCKCKYSNK  311
QY      281  ALPAPIETISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIADVEMESNG  340
Db      318  ALPAPIETISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIADVEMESNG  377
QY      341  PENNYKTPRPVLDSGSFELSKTLVYKSRMOQGNVYSCSYMHALNHNHYOKSLSPG  400
Db      378  PENNYKTPRPVLDSGSFELSKTLVYKSRMOQGNVYSCSYMHALNHNHYOKSLSPG  437

```

RESULT 4
 US-08-494-574-11
 Sequence 11, Application US/08494574
 Patent No. 5783665
 GENERAL INFORMATION:
 APPLICANT: Baum, Peter
 APPLICANT: Goodwin, Ray
 APPLICANT: Fanslow, William
 APPLICANT: Gayle, Richard
 TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
 TITLE OF INVENTION: OX40
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/494, 574

```

? FILLING DATE: 22-JUN-1995
? ..CLASSIFICATION: 530
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/097,822
? FILING DATE: 23-JUL-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Perkins, Patricia A.
? REGISTRATION NUMBER: 34,693
? REFERENCE/DOCKET NUMBER: 2806
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 206-587-0730
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 438 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-494-574-11

```

| | | | | |
|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 59.58% | Score 1332; | DB 1; | Length 438; |
| Best Local Similarity | 62.48% | Pred. No. 1,1e-103; | | |
| Matches 262; | Conservative 23; | Mismatches 75; | Indels 60; | Gaps 6 |

| | | | |
|----|-----|--|-----|
| Oy | 20 | CDKCPGTYLHOHTAKWTKYCACPPHYIYD--SWMTSBECLTCSYVCELOQVKECN | 77 |
| Db | 39 | CREOCPGGMNRRDHDHRLDLCHCEGTFYEANVNDYTCQOCTQCNH--RSGSELKONCT | 96 |
| Oy | 78 | RTHNRCVCEKEGRYLEIFELCKHNSCPPEGVQAGTPERNVYCKRCPDGFSSNETSKA | 137 |
| Db | 97 | PTDPTVCHCR-----PGTPRQDSGKYLVDVCPGPCPHFS--PENNQ | 137 |
| Oy | 138 | PCRKHTNCSVGLLTLTKGNATHONICSGNS-----EST | 171 |
| Db | 138 | ACKPWTNCTLSGKQTRHAPSISDLAVCEDRLATLMTQRPTRPTVQOSTWBPRTS | 197 |
| Oy | 172 | -----QKDYKTHPCPCPAPELLGGPSVLEFPKPKDITMSRTPEVTCVAVDY | 220 |
| Db | 198 | ELPSTPLVYERSCDKHHTCCPCAPAREAGAPSVFLRPRKPDITMSRTPEVTCVAVDY | 257 |
| Oy | 221 | SHEDEYVFNMYVDGVEYHNAKTRPREOYNSTRVYVSYLTVLHQDMLNGREYCKVSNK | 280 |
| Db | 258 | SHEDEYVFNMYVDGVEYHNAKTRPREOYNSTRVYVSYLTVLHQDMLNGREYCKVSNK | 317 |
| Oy | 261 | ALPAPIETKSKAGQRPREPOYTLTPPSRDELTKNOYSLTCLYKAGTSPSIDIAEWBESNQ | 340 |
| Db | 318 | ALPAPIETKSKAGQRPREPOYTLTPPSRDELTKNOYSLTCLYKAGTSPSIDIAEWBESNQ | 377 |
| Oy | 341 | PENNYKTPPLVLDSDGSFYLTKLTVYKSRMQQSNVYSCSMHEALNNHTQKSLSLSPG | 400 |
| Db | 378 | PENNYKTPPLVLDSDGSFYLTKLTVYKSRMQQSNVYSCSMHEALNNHTQKSLSLSPG | 437 |

US-08 5
US-08-464-438-10
Sequence 10, Application US/08484438
Patent No. 581098
Patent No. 581098 5780031
GENERAL INFORMATION:
APPLICANT: Plozman, Gregory D.
APPLICANT: Cuiousscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegal, Clay B.
APPLICANT: Hellstr m, Ingegard
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HERD HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 115 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

```

      ZIP: 10036-2711
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/484,438
      FILING DATE: 07-JUN-1995
      CLASSIFICATION: 530
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/323,442
      FILING DATE: 14-OCT-1994
      APPLICATION NUMBER: US 08/150,704
      FILING DATE: 10-NOV-1993
      CLASSIFICATION: 530
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/981,165
      FILING DATE: 24-NOV-1992
      CLASSIFICATION: 530
      ATTORNEY/AGENT INFORMATION:
      NAME: Mistrock, S. Leslie
      REGISTRATION NUMBER: 18,872
      REFERENCE/DOCKET NUMBER: 5624-230
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 790-9090
      TELEFAX: (212) 869-8864/9741
      TELEX: 66141 PENNIE
      INFORMATION FOR SEQ ID NO: 10:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 911 amino acids
      TYPE: amino acid
      STRANDEDNESS: unknown
      TOPOLOGY: unknown
      MOLECULE TYPE: protein
      US-08-484-438-10

Query Match      56.5%; Score 1266.5; DB 2; Length 911;
Best Local Similarity 59.6%; Pred. No. 9e-98;
Matches 267; Conservative 23; Mismatches 49; Indels 109; Gaps 16;

      31 QACTAKMTVCAPCPDHYTDS--WHTS-DECLYC-----SPVCKELQYVQECNRTNHR 82
      494 ENCRAE-GMVC-----NHLCSDDGCMGPGPDGCLSGRRSRGRICE----- 534
      83 VCECKEGRYLEIEF--PCLAKRSCPPGFGVQAGT-----PERNTVC-----K 122
      535 SCNLYDEDEFERENGSLICE---CDPOCEKMEGDLTCHGPGPNCTCSHFKDGPNCE 591
      123 RCPDGF-----FSNETSKAPCRKHTNCSVFGLLTQ--KGNATHDNI---CSGNS 168
      592 KCPDGLGANSFIKIKADPDRECHPC--HPNC-----TGGCMGPTSHDCLTYIPWTGHS 642
      169 -----ESTOKVDRKTHCCPCPAPABELLGP 192
      643 TLDPDVKVKALEGFPLVGPDFGCAEPANTFLDPEPKSCDKTHCCPCPAPABELLGP 702
      193 SVLFPPPKPCKDLMISRTPEYCVVDYSHDDPEVKKMYVDGYEVHNAKTKPREBOYNS 252
      703 SVLFPPPKPCKDLMISRTPEYCVVDYSHDDPEVKKMYVDGYEVHNAKTKPREBOYNS 762
      253 TYRVASVLTIVHOMLNKEKCKVSNKALPAPTEKTSKAKGPREBOYVTLPPSRDEL 312
      763 TYRVASVLTIVHOMLNKEKCKVSNKALPAPTEKTSKAKGPREBOYVTLPPSRDEL 822
      313 TKNOVSLTCLVKGFPSPDIAEWESNGOPENNKTTPPVLDSDGSFLLYSKLITVDKSMQ 372
      823 TKNOVSLTCLVKGFPSPDIAEWESNGOPENNKTTPPVLDSDGSFLLYSKLITVDKSMQ 882
      373 QGNVSCSVMHALHNHYTKRSLSPG 400
      883 QGNVSCSVMHALHNHYTKRSLSPG 910

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      RESULT 6
      US-08-957-063-16
      Sequence 16, Application US/08957063
      Patent No. 6025157
      GENERAL INFORMATION:
      APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
      TITLE OF INVENTION: Neurturin Receptor
      NUMBER OF SEQUENCES: 19
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Genentech, Inc.
      STREET: 1 DNA Way
      CITY: South San Francisco
      STATE: California
      COUNTRY: USA
      ZIP: 94080
      COMPUTER READABLE FORM:
      MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: MapMatin (Genentech)
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/957,063
      FILING DATE: 24-Oct-1997
      CLASSIFICATION: 800
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/871
      FILING DATE: 9-Jun-1997
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 913
      FILING DATE: 18-Feb-1997
      REFERENCE/DOCKET NUMBER: P1086P2
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 650/952-9881
      TELEFAX: 650/952-9881
      NAME: Torchia, Ph.D., Timothy E.
      REGISTRATION NUMBER: 36,700
      REFERENCE/DOCKET NUMBER: P1086P2
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 650/952-9881
      TELEFAX: 650/952-9881
      INFORMATION FOR SEQ ID NO: 16:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 664 amino acids
      TYPE: Amino Acid
      TOPOLOGY: Linear
      US-08-957-063-16

Query Match      55.8%; Score 1249.5; DB 3; Length 664;
Best Local Similarity 63.6%; Pred. No. 1.6e-96;
Matches 264; Conservative 23; Mismatches 57; Indels 71; Gaps 14;

      32 HCTAKMTVCAPCP-DHY-----YTDSWHTSDECLYCSPVCKELQYV 72
      274 NCRASYTVTS-CPADYQAAGLSYAGMIGFDMTPNYVDSPTG---TVVSPMC----- 323
      73 KOECNRTNHRVCECKEGRYLEIEF---CLKH-----RSCP--PGFVVOAGTP 115
      324 --SCRGSGNNEEBE--KFLR-DFTENPCLRNALQAFNGTGVNVSKGSPFATQAPRV 378
      116 ERNTVRCRCPDGFSSNETSKAPCRKHTNCSVFGLLTQKGNATHD-----NICS 165
      379 EKT---PSLPDDLSDSTSLGTSVITCTSVQEOGL-----KANNSKELSMCFELTNIIP 431
      166 GNSESTOKVKTHTCPCPAPABELLGGSVLFPKPKDITMISRTPEYCVVDYSHEDP 225
      432 GPRD---F-DKTHCCPCPAPABELLGGSVLFPKPKDITMISRTPEYCVVDYSHEDP 488
      226 EVKFNMTVDQVEVHNAKTKRECYNSTYRVSVLTIVHOMLNKEKCKVSNKALPAP 285
      489 EVKFNMTVDQVEVHNAKTKRECYNSTYRVSVLTIVHOMLNKEKCKVSNKALPAP 548
      286 IEKTSKAKGPREBOYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAEWESNGOPENN 345

```

Db 549 IEKTSKAGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSPDIWEMESNGOPENNY 608
QY 346 KTTTPVLDSDGSFFLYSKLTVDKSRMOQGNVSCSYMHGALHNYTOKSLSLSPG 400
Db 609 KTTTPVLDSDGSFFLYSKLTVDKSRMOQGNVSCSYMHGALHNYTOKSLSLSPG 663

RESULT 7

US-08-957-063-18
Sequence 18, Application US/08957063
Patent No. 6025157

GENERAL INFORMATION:

APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
TITLE OF INVENTION: Neurturin Receptor
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,063
FILING DATE: 24-Oct-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871
FILING DATE: 9-Jun-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 913
FILING DATE: 18-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 664 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
08-957-063-18

Query Match 55.7%; Score 1248.5; DB 3; Length 664;
Best Local Similarity 62.7%; Pred. No. 1.9e-96;
Matches 261; Conservative 21; Mismatches 61; Indels 73; Gaps 11;

QY 32 HCTAKMTVCAPCP-DHY-----YTDSWHTSDECLCYSPVCKELQYV 72
Db 274 NCRASYSRTIS-CPADNYOACLSYAGWIGFDMTPNYVDSNPTG---IVVSPFC----- 323
QY 73 KQECNRTNHRVCECKE-----GRYLEIEFCLKHSRCPGFVQAGT 114
Db 324 --NCRSGNNEEBCLEKLRDFTENPCLRNIAQAFNGTDMVMSKPSLP---ATQAPR 377
QY 115 PERNTVCKRCPDGFFSNSTSKAPCRKHTNCSVFGLLTOKGNATHD-----NIC 164
Db 378 VEKT---PSLPDLSDSFSLGTSVITTCSTIQEGL-----KANSKELSMGFTELTNIS 430
QY 165 SGNESSTOKVDKHTCPCRPAPPELLGSPVLFPPKPKDTLMISRTPEVTCVVDVSHED 224
Db 431 PG---SDPVPDHTCPCRPAPPELLGSPVLFPPKPKDTLMISRTPEVTCVVDVSHED 487
QY 225 PEVFNMYVDGVEVHNKTKPREQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPA 284

Db 488 PEVFNMYVDGVEVHNKTKPREQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPA 547
QY 285 PIEKTSKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGOPENN 344
Db 548 PIEKTSKAGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSPDIWEMESNGOPENN 607

QY 345 YKTTTPVLDSDGSFFLYSKLTVDKSRMOQGNVSCSYMHGALHNYTOKSLSLSPG 400
Db 608 YKTTTPVLDSDGSFFLYSKLTVDKSRMOQGNVSCSYMHGALHNYTOKSLSLSPG 663

RESULT 8

US-08-897-236-23
Sequence 23, Application US/08897236A
Patent No. 6075007

GENERAL INFORMATION:

APPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Modified Dorsal Tissue Affecting Factor and Composition
FILE REFERENCE: REG 133
CURRENT APPLICATION NUMBER: US/08/897,236A
CURRENT FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 449
TYPE: PRT
ORGANISM: human
US-08-897-236-23

Query Match 55.5%; Score 1243.5; DB 3; Length 449;
Best Local Similarity 73.7%; Pred. No. 2.9e-96;
Matches 244; Conservative 9; Mismatches 17; Indels 61; Gaps 7;

QY 90 RYLEIEFCLHRSQCPGFGVAGTPEPNTVCK-----RCPDGF 129
Db 159 RYVAVGSCFSKRSK-----SVPE-GAVCKPSKSVHLTLBRKCRQGGQRC--GWI 206
QY 130 SNETSKAPCRKHTNCSVFGLLTOKGNATHDNCSSSESTOKVDKHTCPCRPAPELL 189
Db 207 PIQPIIASEK-----CSG-----DKTHICPPAPABELT 237
QY 190 GGPSPVLFPPKPKDTLMISTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQ 249
Db 238 GGPSPVLFPPKPKDTLMISTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQ 297
QY 250 YNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAGQPREPOVYTLPPSR 309
Db 298 YNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAGQPREPOVYTLPPSR 357
QY 310 DELTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS 369
Db 358 EEMTKNOVSLTCLVKGFPSPDIWEMESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS 417
QY 370 RMOQGNVSCSYMHGALHNYTOKSLSLSPG 400
Db 418 RMOQGNVSCSYMHGALHNYTOKSLSLSPG 448

RESULT 9
US-08-470-299-4
Sequence 4, Application US/08470299
Patent No. 5783181
GENERAL INFORMATION:
APPLICANT: Browne, Michael J.
APPLICANT: Murphy, Kay E.
APPLICANT: Chapman, Conrad G.
APPLICANT: Clinkenberg, Helen E.
APPLICANT: Young, Peter R.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Smithkline Beecham Corporation
 STREET: 709 Swedeland Road, P.O. Box 1539
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,299
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sutton, Jeffrey A.
 REGISTRATION NUMBER: 34,028
 REFERENCE/DOCKET NUMBER: P31005C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5024
 TELEFAX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 387 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-470-299-4

Query Match 55.4%; Score 1240.5; DB 1; Length 387;
 Best Local Similarity 95.8%; Pred. No. 4.3e-96;
 Matches 230; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
 Oy 161 DNICGSGSESTOKVHTKPCPCPAPPELLGSPVFLFPKPKDTLMTSTPEVTCVVDV 220
 Db 148 DSKCSGTE-PSADKTHKPCPCPAPPELLGSPVFLFPKPKDTLMTSTPEVTCVVDV 206
 Oy 221 SHEDEVEKNMYVDGVEVHNATKPREEOYNSTYRVSVLTVLHODWLNKKEYCKKVSNK 280
 Db 207 SHEDEVEKNMYVDGVEVHNATKPREEOYNSTYRVSVLTVLHODWLNKKEYCKKVSNK 266
 Oy 281 ALPALEKTIKSAKOPREPOVYTLPPSRDELTKNOVSLTCLVKGYPYSDIAVEMESNQ 340
 Db 267 ALPALEKTIKSAKOPREPOVYTLPPSRDELTKNOVSLTCLVKGYPYSDIAVEMESNQ 326
 Oy 341 PENNYKTPPVLDSDGSEFLYSLKLTVDKSRMOQGNVFCSVNHEALHNHYTOKSLSPG 400
 Db 327 PENNYKTPPVLDSDGSEFLYSLKLTVDKSRMOQGNVFCSVNHEALHNHYTOKSLSPG 386

RESULT 10
 PCT-US96-10043-9
 Sequence 9, Application PC/TUS9610043
 GENERAL INFORMATION:
 APPLICANT: The General Hospital Corporation
 TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02210-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10043
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,213
 FILING DATE: 14-JUN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lech, Karen F.
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 00786/284001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 442 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-10043-9

Query Match 55.3%; Score 1238.5; DB 4; Length 442;
 Best Local Similarity 89.0%; Pred. No. 7.5e-96;
 Matches 235; Conservative 6; Mismatches 14; Indels 9; Gaps 2;
 Oy 142 HTNCSEFGLLTOKGNATHDNICGSESTOKV-----DKTHTCPCPAPPELLGSPVFL 196
 Db 182 HT-----FPAVQSSGLSVLSSVTVTPSSDKKVEPKSDKTHTCPCPAPPELLGSPVFL 237
 Oy 197 FPKPKDTLMTSRPEVTCVVDVSHEDPEYKFMWYVDGVEVHNATKPREEOYNSTYRV 256
 Db 238 FPKPKDTLMTSRPEVTCVVDVSHEDPEYKFMWYVDGVEVHNATKPREEOYNSTYRV 297
 Oy 257 VSVLTVLHODWLNKKEYCKKSNKALPALEKTIKSAKOPREPOVYTLPPSRDELTKNO 316
 Db 298 VSVLTVLHODWLNKKEYCKKSNKALPALEKTIKSAKOPREPOVYTLPPSRDELTKNO 357
 Oy 317 VSLTCLVKGYPYSDIAVEMESNQGPENNYKTPPVLDSDGSEFLYSLKLTVDKSRMOQGNV 376
 Db 358 VSLTCLVKGYPYSDIAVEMESNQGPENNYKTPPVLDSDGSEFLYSLKLTVDKSRMOQGNV 417
 Oy 377 FSCSVNHEALHNHYTOKSLSPG 400
 Db 418 FSCSVNHEALHNHYTOKSLSPG 441

RESULT 11
 US-08-784-512-3
 Sequence 3, Application US/08784512
 Patent No. 5872209
 GENERAL INFORMATION:
 APPLICANT: BARTNIK, Eckart
 APPLICANT: EIDENMUELLER, Bernd
 APPLICANT: BOETTNER, Frank
 APPLICANT: CATERSON, Bruce
 APPLICANT: HUGHES, Clare
 TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
 TITLE OF INVENTION: and native aggregan to study the proteolytic activity of
 "Aggrecanase" in cell culture systems
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: Suite 500, 3000 K Street, N.W.
 CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,861
FILING DATE: 21-OCT-1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., JR.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B1S1C1P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-940-861-43

```

[illegible]

STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,512
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-512-43

Query Match 55.2%; Score 1237; DB 1; Length 347;
Best Local Similarity 89.7%; Pred. No. 7.3e-96;
Matches 235; Conservative 2; Mismatches 11; Indels 14; Gaps 2;

QY 153 TQKGNATHDNICSG-----NSESTOK---VDKTHCPCPAPPELLGSPVFLFP 198
DB 85 TVSGSLITINLTSDEDEYEMESPNTIDMKFFLYVDKTHCPCPAPPELLGSPVFLFP 144
QY 199 PKPKDTLMISRPEVTCVAVVYSHEDPEVKFNWYDGVGVHNAKTKPREEOYNSTYRVS 258
145 PKPKDTLMISRPEVTCVAVVYSHEDPEVKFNWYDGVGVHNAKTKPREEOYNSTYRVS 204
QY 259 VLTIVHOMLNKEKCKVSKNKPAPRIEKTISKAKGPREPOVYTLPPSRDELTKNOVS 318
DB 205 VLTIVHOMLNKEKCKVSKNKPAPRIEKTISKAKGPREPOVYTLPPSRDELTKNOVS 264
QY 319 LTCLVKGFPSPDIAVWESNGOPENNYKTPPYLDSGSEFLYSKLTVDKSRMOOGNVS 378
DB 265 LTCLVKGFPSPDIAVWESNGOPENNYKTPPYLDSGSEFLYSKLTVDKSRMOOGNVS 324
QY 379 CSVMHEALHNHTOKSLSPG 400
DB 325 CSVMHEALHNHTOKSLSPG 346

RESULT 14
US-08-459-657-43
Sequence 43, Application US/08459657
Patent No. 5914111
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
FUNCTION ASSOCIATED ANTIGEN 3

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,657
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-657-43

Query Match 55.2%; Score 1237; DB 2; Length 347;
Best Local Similarity 89.7%; Pred. No. 7.3e-96;
Matches 235; Conservative 2; Mismatches 11; Indels 14; Gaps 2;

QY 153 TQKGNATHDNICSG-----NSESTOK---VDKTHCPCPAPPELLGSPVFLFP 198
DB 85 TVSGSLITINLTSDEDEYEMESPNTIDMKFFLYVDKTHCPCPAPPELLGSPVFLFP 144
QY 199 PKPKDTLMISRPEVTCVAVVYSHEDPEVKFNWYDGVGVHNAKTKPREEOYNSTYRVS 258
DB 145 PKPKDTLMISRPEVTCVAVVYSHEDPEVKFNWYDGVGVHNAKTKPREEOYNSTYRVS 204
QY 259 VLTIVHOMLNKEKCKVSKNKPAPRIEKTISKAKGPREPOVYTLPPSRDELTKNOVS 318
DB 205 VLTIVHOMLNKEKCKVSKNKPAPRIEKTISKAKGPREPOVYTLPPSRDELTKNOVS 264
QY 319 LTCLVKGFPSPDIAVWESNGOPENNYKTPPYLDSGSEFLYSKLTVDKSRMOOGNVS 378
DB 265 LTCLVKGFPSPDIAVWESNGOPENNYKTPPYLDSGSEFLYSKLTVDKSRMOOGNVS 324
QY 379 CSVMHEALHNHTOKSLSPG 400
DB 325 CSVMHEALHNHTOKSLSPG 346

RESULT 15
US-08-460-132-43
Sequence 43, Application US/08460132
Patent No. 5928643
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.

Search completed: December 27, 2000, 10:53:56
Job time: 147 sec

APPLICANT: WALINER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,132
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,861
FILING DATE: 21-OCT-1992
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-132-43

Query Match 55.2%; Score 1237; DB 2; Length 347;
Best Local Similarity 89.7%; Pred. No. 7.3e-96;
Matches 235; Conservative 2; Mismatches 11; Indels 14; Gaps 2;

QY 153 TQKGNATHNICG-----NSESTOK---VDKTHTCPPAPELGSPVFLFP 198
DB 85 TVSGSLTIINLTSSDDEYEMESPNTDTMKFPLYVDKTHTCPPAPELGSPVFLFP 144

QY 199 PKPKDTLMSRPEPTVCVVVDSHEDPEVAFNNYVDGVEVHNNAKTRPREOYNSTRVVS 258
DB 145 PKPKDTLMSRPEPTVCVVVDSHEDPEVAFNNYVDGVEVHNNAKTRPREOYNSTRVVS 204

QY 259 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNOVS 318
DB 205 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNOVS 264

QY 319 LITCLVGFPSDIAVEMESGQPENNYKTPPYLDSGSEFLYSKLTVDKSRMOQGNVES 378
DB 265 LITCLVGFPSDIAVEMESGQPENNYKTPPYLDSGSEFLYSKLTVDKSRMOQGNVES 324

QY 379 CSVMHEALHNHYTQKSLSLSPG 400
DB 325 CSVMHEALHNHYTQKSLSLSPG 346

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:54:37 ; Search time 40.66 Seconds
(without alignments)
624.301 Million cell updates/sec

Title: US-09-389-545-5

Perfect score: 2240

Sequence: 1 ETPEPKYLHDETSQQLC.....VMHDLNHYTQKSLSPG 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : PIR_65:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1234 | 55.1 | 330 | 1 | IGHU |
| 2 | 1230 | 54.9 | 374 | 2 | Ig gamma-1 chain C |
| 3 | 1229 | 54.9 | 255 | 4 | Ig heavy chain V r |
| 4 | 1225 | 54.7 | 374 | 2 | Ig gamma-1 chain C |
| 5 | 1183.5 | 52.8 | 234 | 2 | Ig heavy chain V r |
| 6 | 1154.5 | 51.5 | 377 | 2 | Ig gamma-3 chain C |
| 7 | 1152.5 | 51.5 | 377 | 2 | Ig gamma-3 chain C |
| 8 | 1148.5 | 51.3 | 326 | 1 | Ig gamma-2 chain C |
| 9 | 1136 | 50.7 | 327 | 1 | Ig gamma-2 chain C |
| 10 | 1133.5 | 50.6 | 289 | 1 | Ig gamma-4 chain C |
| 11 | 923 | 41.2 | 323 | 1 | Ig gamma-3 heavy C |
| 12 | 917.5 | 41.0 | 328 | 2 | Ig gamma chain C r |
| 13 | 917.5 | 41.0 | 328 | 2 | Ig gamma 2b chain |
| 14 | 915.5 | 40.9 | 328 | 2 | Ig gamma 2a chain |
| 15 | 904.5 | 40.4 | 329 | 1 | Ig gamma 4 chain C |
| 16 | 895.5 | 40.0 | 328 | 2 | Ig gamma-2 chain C |
| 17 | 889.5 | 39.7 | 328 | 2 | Ig gamma-1 chain C |
| 18 | 861.5 | 38.5 | 470 | 2 | Ig gamma 3 chain c |
| 19 | 851.5 | 38.0 | 308 | 2 | Ig heavy chain pre |
| 20 | 851.5 | 38.0 | 472 | 2 | Ig heavy chain C r |
| 21 | 847.5 | 37.8 | 329 | 1 | Ig gamma-1 chain C |
| 22 | 843 | 37.6 | 333 | 2 | Ig gamma-3 chain C |
| 23 | 841.5 | 37.6 | 398 | 1 | Ig gamma-2b chain |
| 24 | 830 | 37.1 | 444 | 1 | Ig gamma-3 chain C |
| 25 | 820 | 36.6 | 324 | 1 | Ig gamma-1 chain C |
| 26 | 820 | 36.6 | 326 | 2 | Ig gamma-1 chain C |
| 27 | 820 | 36.6 | 336 | 1 | Ig gamma-1 chain C |
| 28 | 812.5 | 36.3 | 330 | 1 | Ig gamma-2a chain |
| 29 | 812.5 | 36.3 | 399 | 1 | Ig gamma-2a chain |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 812.5 | 36.3 | 469 | 2 | S37483 | Ig gamma-2a chain |
| 31 | 804.5 | 35.9 | 329 | 2 | S00847 | Ig gamma-2c chain |
| 32 | 802.5 | 35.8 | 446 | 2 | S40295 | Ig gamma-2a chain |
| 33 | 801.5 | 35.8 | 335 | 1 | G2MSAB | Ig gamma-2a chain |
| 34 | 791 | 35.3 | 322 | 2 | PS0019 | Ig gamma-2a chain |
| 35 | 777.5 | 34.7 | 336 | 1 | G2MS11 | Ig gamma-2b chain |
| 36 | 777.5 | 34.7 | 405 | 1 | G2MSBW | Ig gamma-2b chain |
| 37 | 777.5 | 34.7 | 474 | 2 | S25057 | Ig gamma-2b chain |
| 38 | 766 | 34.2 | 327 | 2 | S06611 | Ig gamma-2 chain C |
| 39 | 755.5 | 33.7 | 475 | 2 | S01321 | Ig gamma-2b chain |
| 40 | 702 | 31.3 | 180 | 2 | I46732 | Ig gamma heavy cha |
| 41 | 574.5 | 25.6 | 218 | 2 | A36040 | Ig heavy chain V-I |
| 42 | 572.5 | 25.6 | 249 | 2 | S69340 | Ig heavy chain VHI |
| 43 | 566 | 25.3 | 152 | 2 | S14236 | Ig gamma-1 chain C |
| 44 | 397.5 | 17.7 | 572 | 2 | B46529 | Ig y heavy chain (|
| 45 | 374 | 16.7 | 549 | 2 | S04845 | Ig heavy chain pre |

ALIGNMENTS

RESULT 1

IGHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELD>
A:Cross-references: EMBL:217370
A:Note: this sequence has the Gln(17) allelotypic marker, 97-Lys, and the Gln(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:217370
R:Itakhashi, N.; Ueda, S.; Ohta, M.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:217370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024
A:Accession: B90563
A:Contents: myeloma protein Eu
A:Molecule type: protein
A:Residues: 1-96, 'R', '98-135 <GUN>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', '156-165, 'Q', '167-176, 'Q', '178-194, 'N', '196-197, 'D', '199-238, 'E', '2
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Ponting, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein NI

igen primarstruktur.
A:Reference number: A91668; MUID:77070269.
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hope-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primarstruktur des Kristallisierten monoklonalen Immunglobulins IgG1 KO1
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KO1; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'W', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Diexer, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hope-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
embionide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1, 114/1, 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-306/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 55.1%; Score 1234; DB 1; Length 330;
Best Local Similarity 92.1%; Pred. No. 1.2e-68;
Matches 22; Conservative 4; Mismatches 6; Indels 10; Gaps 2;

QY 159 THDNICS-----GNSESNOKY-----DKTHCPCPAPPELLGGPSVFLFPPPKPDTLMIS 208
DB 78 TQYTCVNVNHPKSTKDKKVEPSCDTHCPCPAPPELLGGPSVFLFPPPKPDTLMIS 137
QY 209 RTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNSTYRVSVLTVDHOMWL 268
DB 138 RTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNSTYRVSVLTVDHOMWL 197
QY 269 NGKEYKCKVSKALPAPIEKTISKAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGFP 328
DB 198 NGKEYKCKVSKALPAPIEKTISKAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGFP 257
QY 329 SDIAVESNGQPPNNKTPPVLDSDGSFELYSKLTVDSKRMQGNVFCSSVHEDLHN 388
DB 258 SDIAVESNGQPPNNKTPPVLDSDGSFELYSKLTVDSKRMQGNVFCSSVHEDLHN 317
QY 389 HYTOKSLSLSPG 400
DB 318 HYTOKSLSLSPG 329

RESULT 2
S72664
Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C:Accession: S72664
R:Khamlich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RNA>
A:Cross-references: EMBL:X81695
C:Superfamily: Immunoglobulin C region; immunoglobulin homology

Query Match 54.9%; Score 1230; DB 2; Length 374;
Best Local Similarity 93.1%; Pred. No. 2.5e-68;
Matches 228; Conservative 4; Mismatches 9; Indels 4; Gaps 1;

QY 156 GNATHDNICGNSGNSQKVDKTHCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTC 215
DB 133 GGGTLTVCS-----EPKSCDTHCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTC 188
QY 216 VVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNSTYRVSVLTVDHOMWNGKEYKC 275
DB 189 VVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNSTYRVSVLTVDHOMWNGKEYKC 248
QY 276 KVSNNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGFPSDIAVEW 335
DB 249 KVSNNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGFPSDIAVEW 308
QY 336 ESNQGPENNNKTPPVLDSDGSFELYSKLTVDSKRMQGNVFCSSVHEDLHNHYTOKSL 395
DB 309 ESNQGPENNNKTPPVLDSDGSFELYSKLTVDSKRMQGNVFCSSVHEDLHNHYTOKSL 368
QY 396 SLSPG 400
DB 369 SLSPG 373

RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene produc
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FLV>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-25/Region: human Ig gamma-1 chain C region

Query Match 54.9%; Score 1229; DB 4; Length 255;
Best Local Similarity 98.3%; Pred. No. 1.9e-68;
Matches 226; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 171 TQYKDKTHCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFN 230
DB 25 KSCDCKTHCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFN 84
QY 231 WYVDGVEVHNATKPREEOYNSTYRVSVLTVDHOMWNGKEYKCKVSKALPAPIEKT 290
DB 85 WYVDGVEVHNATKPREEOYNSTYRVSVLTVDHOMWNGKEYKCKVSKALPAPIEKT 144
QY 291 SKAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGFPSDIAVESNGQPPNNKTPP 350

Db 145 SKAAGPREQVYTLPPSRDELTKNOVSLCLVKGFFPSDIAVWESNGOPENNYKTPP 204

QY 351 VLDSGSEFLYKSLTVKSRMOQGNVSCSVMEALHNHYTOKSLSPG 400

Db 205 VLDSGSEFLYKSLTVKSRMOQGNVSCSVMEALHNHYTOKSLSPG 254

RESULT 4

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000

C:Accession: S69339

R:Khamlich, A.A.; Aucuttier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 225, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687

A:Accession: S69339

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

C:Cross-references: EMBL:X81695

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

Query Match 54.7%; Score 1225; DB 2; Length 374;

Best Local Similarity 96.6%; Pred. No. 5e-68;

Matches 225; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 168 SESTQKVDKHTCPCPAPPELLGSPVFLFPPKPKDTLMSRTPEVTCVVDVSHEDPEV 227

Db 141 SSEKSCDKHTCPCPAPPELLGSPVFLFPPKPKDTLMSRTPEVTCVVDVSHEDPEV 200

QY 228 KFNMYVDGVEVHNNAKTRPREQYNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIE 287

Db 201 KFNMYVDGVEVHNNAKTRPREQYNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIE 260

QY 288 KITSKAGPREQVYTLPPSRDELTKNOVSLCLVKGFFPSDIAVWESNGOPENNYKT 347

Db 261 KITSKAGPREQVYTLPPSRDELTKNOVSLCLVKGFFPSDIAVWESNGOPENNYKT 320

QY 348 TPVYLDSDGSEFLYKSLTVKSRMOQGNVSCSVMEALHNHYTOKSLSPG 400

Db 321 TPVYLDSDGSEFLYKSLTVKSRMOQGNVSCSVMEALHNHYTOKSLSPG 373

RESULT 5

PT0207

Ig gamma chain C region - chimpanzee

C:Species: Pan troglodytes (chimpanzee)

C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999

C:Accession: PT0207

R: Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.

Mol. Immunol. 28, 319-322, 1991

A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.

A:Reference number: PT0207; MUID:91287716

A:Accession: PT0207

A:Molecule type: mRNA

A:Residues: 1-234 <EHR>

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: Immunoglobulin

F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 52.8%; Score 1183.5; DB 2; Length 234;

Best Local Similarity 94.4%; Pred. No. 1.1e-65;

Matches 221; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

QY 170 STOKVNDK-----THTCPPCPAPPELLGSPVFLFPPKPKDTLMSRTPEVTCVVDV 220

Db 1 SNTRVNDKVPKSCDTHTGCPCPAPPELLGSPVFLFPPKPKDTLMSRTPEVTCVVDV 60

QY 221 SHEDPEVKFNMVYDGVVHNNAKTRPREQYNSTYRVVSVLTVLHODWLNGKEYCKVSNK 280

Db 61 SHEDPEVKFNMVYDGVVHNNAKTRPREQYNSTYRVVSVLTVLHODWLNGKEYCKVSNK 120

QY 261 ALPAPIEKITSKAGPREQVYTLPPSRDELTKNOVSLCLVKGFFPSDIAVWESNGQ 340

Db 121 ALPAPIEKITSKAGPREQVYTLPPSRDELTKNOVSLCLVKGFFPSDIAVWESNGQ 180

QY 341 PENNYKTPVYLDSDGSEFLYKSLTVKSRMOQGNVSCSVMEALHNHYTOKS 394

Db 181 PENNYKTPVYLDSDGSEFLYKSLTVKSRMOQGNVSCSVMEALHNHYTOKS 234

RESULT 6

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C:Species: Homo sapiens (man)

C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999

C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:

A:Reference number: A23511; MUID:86148507

A:Accession: A23511

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

A:Cross-references: GB:X03604; GB:M2958; NID:933070; PIDN:CAA27268.1; PID:9577056

C:Genetics:

A:Gene: IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

A:Insertions: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: Immunoglobulin

F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 51.5%; Score 1154.5; DB 2; Length 377;

Best Local Similarity 67.1%; Pred. No. 1e-63;

Matches 228; Conservative 19; Mismatches 32; Indels 61; Gaps 7;

QY 76 CNRTNHRCECKEGRYLEIEF-----CLKHSK---PPGEGVQAGTPERTVC 121

Db 83 CNVNH-KPSMTKVDKRVLELTPTGDTHTGCPCEPERSCTPP-----C 126

QY 122 KCPDGFSEIETSKAP-CKHTNCVFGILLTQKNATHDNIGSSESTQKVDKTHC 180

Db 127 PCPEP-KSCDTPPCPCPEPSC-----DTPPC 156

QY 181 PCPAPPELLGSPVFLFPPKPKDTLMSRTPEVTCVVDVSHEDPEVKFNMVYDGVHN 240

Db 157 PCPAPPELLGSPVFLFPPKPKDTLMSRTPEVTCVVDVSHEDPEVKFNMVYDGVHN 216

QY 241 AKTRPREQYNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKITSKAGPREP 300

Db 217 AKTRPREQYNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIEKITSKAGPREP 276

QY 301 QVYTLPPSRDELTKNOVSLCLVKGFFPSDIAVWESNGOPENNYKTPVYLDSDGSEFL 360

Db 277 QVYTLPPSRDELTKNOVSLCLVKGFFPSDIAVWESNGOPENNYKTPVYLDSDGSEFL 336

QY 361 YSKLTVKSRMOQGNVSCSVMEALHNHYTOKSLSPG 400

Db 337 YSKLTVKSRMOQGNVSCSVMEALHNHYTOKSLSPG 376

RESULT 7

A60764

Ig gamma-3 chain C region, form LAT - human

C:Species: Homo sapiens (man)

C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999

C:Accession: A60764

R:Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

Mol. Immunol. 6, 923-925, 1979

A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G2.

A:Reference number: A93132; MUID:80114419

A:Contents: Zie

A:Accession: A93132

A:Molecule type: Protein

A:Residues: 238-275 <HOR>

R:Hofmann, T.; Parr, D.M.

Submitted to the Atlas, March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A>Note: the revised sequence differs from that shown in having 60-Ala and in the amided

R:Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A>Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; MUID:72033500

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Milstein, C.; Plink, J.R.L.

Nature 221, 145-148, 1969

A>Title: Structural studies of immunoglobulin G.

A:Reference number: A93157; MUID:69064124

A:Contents: annotation; Sa, disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG2

A:Cross-references: GDB:119338; OMIM:147110

A:Map position: 14q32.33-14q32.33

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:133-202/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: Interchain (to light chain) #status experimental

F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental

F:116/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.3%; Score 1148.5; DB 1; Length 326;
Best Local Similarity 90.3%; Pred. No. 2e-63;
Matches 214; Conservative 8; Mismatches 8; Indels 7; Gaps 2;

QY 170 STQVYDKT-----HTCPPCAPPELLGGPSVFLFPPPKPTLMISRPETCVVDYSHE 223
| | | | | : | | | | |
Db 90 SNTFYDVTVERKCCVECPPCPAP-VAGPSVFLEPPKPKDTLMSRPEVTCVVVDVSHE 148

QY 224 DEPYKFMMYDVGVNHNAKTRPREOYNSTRVAVSVTLVHODLNKEVKCKVSKNALP 283
| | | | | : | | | | |
Db 149 DPEVQFMNYDVGVNHNAKTRPREOYNSTRVAVSVTLVHODLNKEVKCKVSKNGLP 208

QY 284 APIKITISKAKGPREFPOVYTLTPSRDELTKNOVSLTCLVKGFPSPDIAMWESNGOPEN 343
| | | | | : | | | | |
Db 209 APIKITISKRTKGPREFPOVYTLTPSRDEMTKNQVSLCLVKGFPSPDIAMWESNGOPEN 268

QY 344 NYKTTPPVLDSDGSFFLYSKLTVDKSRMQQGNWFSCVMHDALHNHYTQKSLSLSPG 400
| | | | | : | | | | |
Db 269 NYKTTPPMVLDSGDSFFLYSKLTVDKSRMQGNWFSCVMHEALHNHYTQKSLSLSPG 325

RESULT 9

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999

C:Accession: A90933; A90249; A02150

R:Elliason, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A>Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104

A:Molecule type: DNA

A:Reference number: A91749; MUID:84030930
 A:Accession: A91749
 A:Molecule type: mRNA
 A:Residues: 1-323 <BERR>
 A:Note: This sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
 R:Pratt, D.M.; Mole, L.E.
 Biochem. J. 151, 337-349, 1975
 A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin
 A:Reference number: A90290; MUID:76135469
 A:Accession: A90290
 A:Molecule type: protein
 A:Residues: 1-47, 'E', '49-71', 'PV', '72-128' <PRA>
 R:Matens, C.L.; Moore, K.W.; Steimetz, M.; Hood, L.; Knight, K.L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
 A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
 A:Reference number: A93928; MUID:83299917
 A:Accession: A93928
 A:Molecule type: mRNA
 A:Residues: 88-103, 'M', '105-143', 'E', '145-184', 'A', '186', 'E', '188-266' <MAR>
 A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker
 R:Frutcher, R.E.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
 Biochem. J. 116, 249-259, 1970
 A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
 A:Reference number: A90245; MUID:70110015
 A:Accession: A90245
 A:Molecule type: protein
 A:Residues: 132-143, 'E', '145-161' <FRU>
 R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
 In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp. 109-127, Almqvist and Wiksell, A:Reference number: A94416
 A:Accession: A94416
 A:Molecule type: protein
 A:Residues: 129-131, '155-172', 'D', '174-184', 'A', '186', 'E', '188-200', 'D', '202-217', 'E', '219-232', 'Q', 'A:Note: This has the e15 allotypic marker. 185-Ala
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-82/Domain: immunoglobulin homology <IM1>
 F:130-199/Domain: immunoglobulin homology <IM2>
 F:236-303/Domain: immunoglobulin homology <IM3>
 F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.2%; Score 923; DB 1; Length 323;
 Best Local Similarity 61.5%; Pred. No. 1.2e-49;
 Matches 177; Conservative 33; Mismatches 46; Indels 32; Gaps 5;

123 RCPDGFES-----NETSSKAPCRKHTNCSVGLLLTQKGNATHDNICSGNSESTOKVDKT 177
 Db 57 RQSGSLVSLSSVSVTSSQ-----VTCNV-----AHPATTKVKVKT 94

178 ---HTC--PPCPAPBELLGSPVFLFPKPKDLMISRPEVTCVVVDVSHEDPEVKFNW 232
 Db 95 VAPSTCSKPTCPPELLGSPVFLFPKPKDLMISRPEVTCVVVDVSHEDPEVKFNW 154

233 VDGEVHNAAKTKPREQVNSTYRVSVLTVLHODMLNGEKVKCKSNKALPAPIETKTSK 292
 Db 155 INNEQVRIARPPLEKQONSTIRVSTLPTTHODMLRKERFKCKVHNKALPAPIETKTSK 214

293 AKQPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIJAVESNGOPENNYKTTPPVL 352
 Db 215 ARGQPLEKRYVTMGPRLRELSRSYSLTCLMNGFPPSDISVEMWENGAEDNYKTTPAVL 274

353 DSDGSFYLKSLTYDKSRMOGQNFSCSVMEALHNHYTQKSLSPG 400
 Db 275 DSDGSFYLKSLTYDKSRMOGQNFSCSVMEALHNHYTQKSLSPG 322

RESULT 12
 147160
 Ig gamma 2b chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: 147160
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
 A:Reference number: 147158; MUID:95015845
 A:Accession: 147158
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03779; NID:9433125; PIDN:AAA52218.1; PID:9433126
 C:Genetics:
 A:Gene: IgG2b
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IM3>

Query Match 41.0%; Score 917.5; DB 2; Length 328;
 Best Local Similarity 60.5%; Pred. No. 2.6e-49;
 Matches 176; Conservative 35; Mismatches 43; Indels 37; Gaps 6;

125 PDGFSNETSSKAPC-----RKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDK---T 177
 Db 59 PSGLYSLSMVTVPASSLSKSTYCNV-----NHPATTKVKDKRVGT 100

178 HTCPPCP-----APBELLGSPVFLFPKPKDLMISRPEVTCVVVDVSHEDPEVKFNW 231
 Db 101 KTKPCPCPCPACESP---GSPVFIFPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNW 156

232 YVDGEVHNAAKTKPREQVNSTYRVSVLTVLHODMLNGEKVKCKSNKALPAPIETKTS 291
 Db 157 YVDGEVHNAAKTKPREQVNSTYRVSVLTVLHODMLNGEKVKCKSNKALPAPIETKTS 216

292 KAKQPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIJAVESNGQ---PENNYKTT 349
 Db 217 KAKQPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIJAVESNGQ---PENNYKTT 276

350 PVLSDGSFYLKSLTYDKSRMOGQNFSCSVMEALHNHYTQKSLSPG 400
 Db 277 PVDVDTGYFLYSKSVDKASWQGGIFQCAVMEALHNHYTQKSLSPG 327

RESULT 13
 147159
 Ig gamma 2a chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: 147159
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
 A:Reference number: 147158; MUID:95015845
 A:Accession: 147159
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
 C:Genetics:
 A:Gene: IgG2a
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IM3>

Query Match 41.0%; Score 917.5; DB 2; Length 328;
 Best Local Similarity 60.5%; Pred. No. 2.6e-49;
 Matches 176; Conservative 35; Mismatches 43; Indels 37; Gaps 6;

125 PDGFSNETSSKAPC-----RKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDK---T 177
 Db 59 PSGLYSLSMVTVPASSLSKSTYCNV-----NHPATTKVKDKRVGT 100

178 HTCPPCP-----APBELLGSPVFLFPKPKDLMISRPEVTCVVVDVSHEDPEVKFNW 231


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Db      101 KTRPPCIPACSP-----GPSVFIPPKPKDLMISRTQVTCVVDVSGQENPEVQFSW 156
      232 YVDGVEVHNKTRPREBOYNSTRVSVLTVLVHODWLNGREYCKCKVSNKALPAPIETKIS 291
      157 YVDGVEVHNKTRPREBOYNSTRVSVLTVLVHODWLNGREYCKCKVSNKALPAPIETKIS 216
      292 KAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTPP 349
      217 KAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTPP 276
      350 PVLDSGSEFLYSKLTVDKSRMOGNGVSCSVNHEALHNHYTOKSLSPG 400
      277 PQDDVDTYLYSKFYDKASWOGGIFQCAVNHMALHNHYTOKSLSPG 327

RESULT 14
I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence: revision 21-Feb-1997 #text-change 21-Jan-2000
Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
F:82-151/Domain: Immunoglobulin homology <IMM>

Query Match      40.9%; Score 915.5; DB 2; Length 277;
Best Local Similarity 61.3%; Pred. No. 2.9e-49;
Matches 176; Conservative 34; Mismatches 48; Indels 29; Gaps 6;

      125 PDGFSSNETSSKAPC---RKHTNCSVFGLLLQKGNATHDNCISGSESTOKYDK--T 177
      8 PSLGLSSKMTVTPASSLSKSTTCNV-----NHPAITTYVDKRVGT 49
      178 HTCPPCP-APELLG-GPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVFNMYVDG 235
      50 KTRPPCIPACSPGPSAFIFPPKPKDLMISRTPEVTCVVDVSGQENPEVQFSWYVDG 109
      236 VEVHNKTRPREBOYNSTRVSVLTVLVHODWLNGREYCKCKVSNKALPAPIETKISKAG 295
      110 VEVHNKTRPREBOYNSTRVSVLTVLVHODWLNGREYCKCKVSNKALPAPIETKISKAG 169
      296 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTPPVD 353
      170 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTPPVD 229
      354 SDGSEFLYSKLTVDKSRMOGNGVSCSVNHEALHNHYTOKSLSPG 400
      230 VQDTYLYSKLTVDKASWOGGIFQCAVNHMALHNHYTOKSLSPG 276

RESULT 15
I47162
Ig gamma-2 chain C region - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-May-1981 #sequence: revision 07-May-1981 #text-change 16-Jul-1999
Accession: A94553; A90352; A90359; A90384; A90385; A02151
R:Trischmann, T.M.
submitted to the Atlas, April 1975
A:Reference number: A94553
A:Accession: A94553
A:Molecule type: protein

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A:Residues: 1-3 <TR>
R:Birshtein, B.K.; Huseaid, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
A:Reference number: A90352; MUID:71058471
A:Accession: A90352
A:Molecule type: protein
A:Residues: 4-68 <BIR>
R:Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II.
A:Reference number: A90359; MUID:71058486
A:Accession: A90359
A:Molecule type: protein
A:Residues: 69-133; 312-329 <TUR>
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974.
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibody
A:Reference number: A90384; MUID:75036072
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibody
A:Reference number: A90385; MUID:75036073
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR2>
R:Oliveira, B.; Lamu, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2 immunoglobulin.
A:Reference number: A90354; MUID:71058474
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: Immunoglobulin homology <IM1>
F:135-204/Domain: Immunoglobulin homology <IM2>
F:241-310/Domain: Immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match      40.4%; Score 904.5; DB 1; Length 329;
Best Local Similarity 60.3%; Pred. No. 1.6e-48;
Matches 173; Conservative 30; Mismatches 53; Indels 31; Gaps 3;

      127 GFSSNETSSKAPCKRTKTSVFGLLLQKGNATHDNCISGSESTOKYDKT----- 177
      61 GLYSLTSMVTVPSSQKATCNV-----AHAPSSTKVTKEVPIPTPAP 102
      178 --HTCPPCAPPELLGSPVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVFNMYVDG 235
      103 BPCTCKPCPPENMGSPSFIFFPKPKDLMISRTPEVTCVVDVSGQENPEVQFTFVDN 162
      296 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTPPVD 353
      223 APMPDPVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTPPVD 282
      354 SDGSEFLYSKLTVDKSRMOGNGVSCSVNHEALHNHYTOKSLSPG 400
      283 ADGSTFLYSKLTVDKASWOGGIFQCAVNHMALHNHYTOKSLSPG 329

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Thu Dec 28 15:09:22 2000

us-09-389-545-5.rpt

Page 8

Search completed: December 27, 2000, 10:54:39
Job time: 190 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:55:05 ; Search time 24.16 Seconds

(without alignments)
528.939 Million cell updates/sec

Title: US-09-389-545-5

Sequence: 1 ETPPKYHLYHDETSQQLC.....VMHEALHNHYTKSLSPG 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-------------|---------------------|
| 1 | 1234 | 55.1 | 330 | 1 GCL_HUMAN | P01857 homo sapien |
| 2 | 1148.5 | 51.3 | 326 | 1 GCL_HUMAN | P01859 homo sapien |
| 3 | 1136 | 50.7 | 327 | 1 GCL_HUMAN | P01861 homo sapien |
| 4 | 1133.5 | 50.6 | 290 | 1 GCL_HUMAN | P01860 homo sapien |
| 5 | 923 | 41.2 | 323 | 1 GCL_HUMAN | P01870 oryctolagus |
| 6 | 904.5 | 40.4 | 329 | 1 GCL_HUMAN | P01862 cavia porce |
| 7 | 847.5 | 37.8 | 329 | 1 GCL_HUMAN | P02761 ratuus norv |
| 8 | 843 | 37.6 | 333 | 1 GCL_HUMAN | P03987 mus musculu |
| 9 | 841.5 | 37.6 | 338 | 1 GCL_HUMAN | P01868 mus musculu |
| 10 | 820 | 36.6 | 324 | 1 GCL_HUMAN | P01869 mus musculu |
| 11 | 820 | 36.6 | 326 | 1 GCL_HUMAN | P01879 mus musculu |
| 12 | 820 | 36.6 | 333 | 1 GCL_HUMAN | P01869 mus musculu |
| 13 | 812.5 | 36.3 | 330 | 1 GCL_HUMAN | P01863 mus musculu |
| 14 | 812.5 | 36.3 | 330 | 1 GCL_HUMAN | P01865 mus musculu |
| 15 | 804.5 | 35.9 | 329 | 1 GCL_HUMAN | P02762 ratuus norv |
| 16 | 801.5 | 35.8 | 335 | 1 GCL_HUMAN | P01864 mus musculu |
| 17 | 791 | 35.3 | 322 | 1 GCL_HUMAN | P20760 ratuus norv |
| 18 | 777.5 | 34.7 | 336 | 1 GCL_HUMAN | P01866 mus musculu |
| 19 | 777.5 | 34.7 | 405 | 1 GCL_HUMAN | P01867 mus musculu |
| 20 | 365.5 | 16.3 | 391 | 1 GCL_HUMAN | P04220 homo sapien |
| 21 | 361 | 16.1 | 421 | 1 GCL_HUMAN | P06336 mus musculu |
| 22 | 360 | 16.1 | 454 | 1 GCL_HUMAN | P01871 homo sapien |
| 23 | 354.5 | 15.8 | 454 | 1 GCL_HUMAN | P01872 mus musculu |
| 24 | 353 | 15.8 | 428 | 1 GCL_HUMAN | P01874 mus musculu |
| 25 | 353 | 15.8 | 428 | 1 GCL_HUMAN | P01874 mus musculu |
| 26 | 349.5 | 15.6 | 476 | 1 GCL_HUMAN | P01875 mus musculu |
| 27 | 345.5 | 15.4 | 461 | 1 GCL_HUMAN | P20333 mus musculu |
| 28 | 340 | 15.2 | 458 | 1 GCL_HUMAN | P03988 oryctolagus |
| 29 | 340 | 15.2 | 474 | 1 GCL_HUMAN | P25119 mus musculu |
| 30 | 338.5 | 15.1 | 450 | 1 GCL_HUMAN | P01874 canis famli |
| 31 | 335 | 15.0 | 479 | 1 GCL_HUMAN | P04221 oryctolagus |
| 32 | 333.5 | 14.9 | 454 | 1 GCL_HUMAN | P06337 mesocricetu |
| 33 | 332.5 | 14.8 | 457 | 1 GCL_HUMAN | P20768 suncus murti |

ALIGNMENTS

| RESULT | ID | STANDARD | PRT | 330 AA. |
|--------|--|----------|-----|---------|
| 1 | GCL_HUMAN | | | |
| 2 | GCL_HUMAN | | | |
| 3 | P01857 | | | |
| 4 | 21-JUL-1986 (Rel. 01, Created) | | | |
| 5 | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| 6 | 15-JUL-1999 (Rel. 38, Last annotation update) | | | |
| 7 | IG GAMMA-1 CHAIN C REGION. | | | |
| 8 | IGH31. | | | |
| 9 | OS Homo sapiens (Human). | | | |
| 10 | OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| 11 | OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| 12 | [1] | | | |
| 13 | SEQUENCE FROM N.A. | | | |
| 14 | RX MEDLINE; 82274238. | | | |
| 15 | RA Ellison J.W., Berson B.J., Hood L.E.; | | | |
| 16 | RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene."; | | | |
| 17 | RL Nucleic Acids Res. 10:4071-4079(1982). | | | |
| 18 | [2] | | | |
| 19 | SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). | | | |
| 20 | RX MEDLINE; 71064024. | | | |
| 21 | RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., | | | |
| 22 | RT Wexel M.J., Edelman G.M.; | | | |
| 23 | RL "The covalent structure of a human gamma G-immunoglobulin. VII. Amino | | | |
| 24 | acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; | | | |
| 25 | RL Biochemistry 9:3161-3170(1970). | | | |
| 26 | [3] | | | |
| 27 | SEQUENCE OF 136-329 (EU). | | | |
| 28 | RX MEDLINE; 71064025. | | | |
| 29 | RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., | | | |
| 30 | RT Edelman G.M.; | | | |
| 31 | RL "The covalent structure of a human gamma G-immunoglobulin. 8. Amino | | | |
| 32 | acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; | | | |
| 33 | RL Biochemistry 9:3171-3181(1970). | | | |
| 34 | [4] | | | |
| 35 | SEQUENCE (MYELOMA PROTEIN NIE). | | | |
| 36 | RX MEDLINE; 77070269. | | | |
| 37 | RA Ponsing H., Hilschmann N.; | | | |
| 38 | RT "The rule of antibody structure. The primary structure of a | | | |
| 39 | monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The | | | |
| 40 | tryptophan residues of the H-chain, alignment of the tryptic | | | |
| 41 | peptides and discussion of the complete structure."; | | | |
| 42 | RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976). | | | |
| 43 | [5] | | | |
| 44 | SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. | | | |
| 45 | RX MEDLINE; 83289131. | | | |
| 46 | RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; | | | |
| 47 | RT "Three-dimensional structure determination of antibodies. Primary | | | |
| 48 | structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; | | | |
| 49 | RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983). | | | |
| 50 | [6] | | | |
| 51 | DISULFIDE BONDS. | | | |
| 52 | RX MEDLINE; 71064027. | | | |
| 53 | RA Gall W.E., Edelman G.M.; | | | |
| 54 | RT "The covalent structure of a human gamma G-immunoglobulin. X. | | | |
| 55 | Intrachain disulfide bonds."; | | | |

Biochemistry 9:3188-3196(1970).

[7] DISULFIDE BONDS.

RP MEDLINE: 77070267.

RA Dreker L., Schwarz J., Relchel W., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nle). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

RT Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

RL [8]

RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).

RX MEDLINE: 81208100.

RA Deisenhofer J.;

RT "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from *Staphylococcus aureus* at 2.9- and 2.8-A resolution.";

RT Biochemistry 20:2361-2370(1981).

CC -I- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3) MARKER & THE GLM (NON-1) MARKERS.

CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155,166,177,195,198,269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.

CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198,267&272.

CC -----

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CC -----

DR EMBL: J00228; AAC82527.1; ALF_INIT.

DR PIR: A02146; GHU.

DR PDB: 1FC1; 15-JUL-92.

DR PDB: 1FC2; 15-JUL-92.

DR MIM: 147100;

DR INTERPRO: IPR000495; -.

DR INTERPRO: IPR003006; -.

DR PRAM: PF00047; 15; 3.

DR PROSITE: PS00290; IG_MHC; 2.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 3D-structure.

FT NON_TER 1 1

FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.

FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330 CH3.

FT DISULFID 27 83

FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFID 144 204

FT DISULFID 250 308

FT CARBOHYD 180 97

FT VARIANT 97 97

FT VARIANT 239 239

FT VARIANT 241 241

FT MOD_RES 330 330

FT STRAND 123 126

FT HELIX 130 134

FT TURN 136 137

FT STRAND 141 148

FT STRAND 158 162

FT TURN 163 164

FT TURN 163 164

FT STRAND 165 166

FT STRAND 175 178

FT STRAND 183 190

FT HELIX 193 197

FT TURN 198 199

FT STRAND 202 206

FT STRAND 215 219

FT STRAND 227 227

FT STRAND 230 234

FT STRAND 238 240

FT HELIX 241 242

FT TURN 241 242

FT STRAND 245 256

FT STRAND 260 266

FT TURN 267 268

FT STRAND 269 270

FT STRAND 274 276

FT STRAND 280 281

FT TURN 283 284

FT STRAND 287 296

FT HELIX 297 301

FT TURN 302 303

FT STRAND 306 312

FT TURN 313 314

FT TURN 316 317

FT STRAND 320 324

SO SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 55.1%; Score 1234; DB 1; Length 330;

Best Local Similarity 92.1%; Pred. No. 7e-77;

Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;

OY 159 THDNCS-----GNSGSKY-----DKTHCPCPAPELLGGSVFLFPKPKDTLMIS 208

DB 78 TQTYCNHNKPSNKKVKKVPEKSCDKTHCPCPAPELLGGSVFLFPKPKDTLMIS 137

OY 209 RPPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAAKTKPREQYNSTRYVSVLTVLHODML 268

DB 138 RPPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAAKTKPREQYNSTRYVSVLTVLHODML 197

OY 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDELTKNOVSLTCLVKGFYP 328

DB 198 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDELTKNOVSLTCLVKGFYP 257

OY 329 SDIAVEWESNQPENNYKTPPEVLDSGSEFLYSLKLTVDKSRMOQGNVFSGVNHEALHN 388

DB 258 SDIAVEWESNQPENNYKTPPEVLDSGSEFLYSLKLTVDKSRMOQGNVFSGVNHEALHN 317

OY 389 HTYOKSLSLSPG 400

DB 318 HTYOKSLSLSPG 329

RESULT 2

GC2_HUMAN STANDARD; PRT; 326 AA.

ID GC2_HUMAN

AC P01859;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG GAMMA-2 CHAIN C REGION.

GN IGHG2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RN [1]

RX MEDLINE: 82197621.

RA Ellison J.W., Hood L.E.;

RT "Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).

[2]

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE; 81007873.
 RA Wang A.-C., Tung E., Fudenberg H.R.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 RL evolutionary, and functional implications.";
 RN J. Immunol. 125:1048-1054(1980).
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE; 80001357.
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RL domains of a human IgG2 myeloma protein.";
 RN Can. J. Biochem. 57:758-767(1979).
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE; 80114419.
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RL Mol. Immunol. 16:923-925(1979).
 RN [5]
 RP REVISIONS TO 25, 59, 60 AND 264-268 (ZIE).
 RX Hofmann T., Parr D.M.;
 RT Submitted (MAR-1980) to the PIR data bank.
 RN [6]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE; 95253298.
 RA Stopini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RL immunoglobulins";
 RN Eur. J. Biochem. 228:886-893(1995).
 RP DISULFIDE BONDS.
 RX MEDLINE; 72033500.
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [8]
 RP DISULFIDE BONDS.
 RX MEDLINE; 69064124.
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 RN -----
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 CC -----
 DR EMBL; V00554; CAA23814.1; -
 DR EMBL; V00554; CAA23815.1; -
 DR EMBL; V00554; CAA23816.1; -
 DR EMBL; V00554; CAA23817.1; -
 DR PIR; A02148; G2HU.
 DR MIM; 147110; -
 DR INTERPRO; IPR000495; -
 DR INTERPRO; IPR003006; -
 DR PIR; A02148; G2HU.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 146 304
 FT VARIANT 60 60
 FT SITE 156 156
 FT MOD_RES 326 326
 SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 Query Match 51.3%; Score 1148.5; DB 1; Length 326;
 Best Local Similarity 90.3%; Pred. No. 4,2e-71;
 Matches 214; Conservative 8; Mismatches 8; Indels 7; Gaps 2;
 QY 170 STOKVDKT-----HICPPAPABELGSPVFLPPPKNDTLMISRTPEVTVVDVSH 223
 DB 90 SNRKVDKVERKCCVEPCPPAPVAGSPVFLPPPKNDTLMISRTPEVTVVDVSH 148
 QY 224 DPEYKENVYDGYVYHNAKTRPREQYNSYRYVSVTLVHOMLNGKEKCKVSNKALP 283
 DB 149 DPEVQFNWYDGVYHNAKTRPREQYNSYRYVSVTLVHOMLNGKEKCKVSNKGLP 208
 QY 284 APIEKTISKAKGPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPEN 343
 DB 209 APIEKTISKAKGPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPEN 268
 QY 344 NYKTPPVLDSDGSFPLYSKLVDRKSRMOGNYFSCSVMEALHNHYTKSLSLSPG 400
 DB 269 NYKTPPVLDSDGSFPLYSKLVDRKSRMOGNYFSCSVMEALHNHYTKSLSLSPG 325
 RESULT 3
 GC4_HUMAN STANDARD; PRT; 327 AA.
 ID GC4_HUMAN
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-4 CHAIN C REGION.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83157104.
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE; 70207560.
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RL constant region of a gamma 4 chain.";
 RN Biochem. J. 117:33-47(1970).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A02150; GAHU.
 DR MIM; 147130; -
 DR INTERPRO; IPR000495; -
 DR INTERPRO; IPR003006; -
 DR PIR; A02150; GAHU.
 DR PROSITE; PS00290; IG_MHC; 2
 DR Immunoglobulin domain; Immunoglobulin C region.

21-JUL-1986 (Rel. 01, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG GAMMA-2 CHAIN C REGION.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriognathli; Caviidae; Cavia.
 RN [1]
 RP SEQUENCE OF 1-3.
 RA Trischmann T.M.;
 RL Submitted (APR-1975) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 4-68.
 RA MEDLINE; 71058471.
 RA Birshrein B.K., Hussain Q.Z., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 immunoglobulin-6(2). 3. Amino acid sequence of the region around the
 half-cysteine joining heavy and light chains.";
 RT Biochemistry 10:18-25(1971).
 RL [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RA MEDLINE; 71058486.
 RA Turner K.J., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 immunoglobulin-6(2). II. Amino acid sequence of the carboxyl-terminal
 and hinge region cyanogen bromide fragments.";
 RT Biochemistry 10:9-17(1971).
 RL [4]
 RP SEQUENCE OF 134-226.
 RA MEDLINE; 75036072.
 RA Tracey D.E., Cebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2
 antibodies.";
 RT Biochemistry 13:4796-4803(1974).
 RL [5]
 RP SEQUENCE OF 227-311.
 RA MEDLINE; 75036073.
 RA Trischmann T.M., Cebra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 antibodies.";
 RT Biochemistry 13:4804-4811(1974).
 RL [6]
 RP DISULFIDE BONDS.
 RA MEDLINE; 71058474.
 RA Oliveira B., Lamm M.E.;
 RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
 RT Biochemistry 10:26-31(1971).
 RL -1 MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
 13 INBRED GUINEA PIGS.
 DR PIR; A02151; G2GP.
 DR INTERPRO; IPR000495; -
 DR INTERPRO; IPR003006; -
 DR PFAM; PF00047; 1g; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 28 79
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 142 202
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
 FT DISULFID 248 308
 FT SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;
 SQ
 Query Match 40.4%; Score 904.5; DB 1; Length 329;
 Best Local Similarity 60.3%; Pred. No. 1.4e-54;
 Matches 173; Conservative 30; Mismatches 53; Indels 31; Gaps 3;
 QY 127 GFSSNETSSKAPCRKHTNCSYFGLLLTQKGNATHDNICSGNSESTQKYDKT-----177
 DB 61 GLYSILTSWTVPSQKATCNV-----AHPASSTKYDKVEPIRTPZP 102

178 --HTCPCPAPBELLGSPVLFPPKPKDTIMISRTPEVTCVVDVSHDEPEVKNMYVDG 235
 DB 103 BPCPCPCPCPPENIGGSVDFEPPKPKDTIMISTPEVTCVVDVSDDEPEVQTPVDN 162
 QY 236 VEVHNAKTPREEOYNSTYRVSVLFTVHODWLNKGRKYSKAPAPAEIKTISKAKG 295
 DB 163 KPVGNNAETKPREVEQNTTFVESVLPFGHODWLNKGRKYSKAPAPAEIKTISKKG 222
 QY 296 QPREPOVYTLPPSHDELTKNQVSLTCLVKGFPSDIAVEESNQGP--ENNYKTPPVLD 353
 DB 223 APRMPDVYTLPPSHDELTKSVSVTCLINFEPPADIVHVASNRPVSEKEKNTPIED 282
 QY 354 SDGSFELYSKLTVDSRWQGVNFCSCVMHEDALHNHTQKSLSPG 400
 DB 293 ADGSYFLYSKLTVDKSSAMDGTVTYCSVMHEDALHNHTQKSLSPG 329
 RESULT 7
 GC3_MOUSE STANDARD; PRT; 329 AA.
 ID GC3_MOUSE
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathli; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 85027161.
 RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner P.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RT EMBO J. 3:2041-2046(1984).
 RL
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 CC
 DR EMBL; J00451; -. NOT_ANNOTATED_CDS.
 DR PIR; B02156; G3MSC.
 DR INTERPRO; IPR000495; -
 DR INTERPRO; IPR003006; -
 DR PFAM; PF00047; 1g; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin C region; Glycoprotein; Transmembrane;
 KW Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 FT SEQUENCE 329 AA; 36228 MW; F45627174182BAD6 CRC64;
 SQ
 Query Match 37.8%; Score 847.5; DB 1; Length 329;
 Best Local Similarity 54.0%; Pred. No. 9.7e-51;
 Matches 162; Conservative 47; Mismatches 72; Indels 19; Gaps 5;
 QY 107 FGVAQAGTPERNIVCKRCPGFFSNETSSKAPCRKHTNCSYFGLLLTQKGNATHDNICSG 166
 DB 42 YGALSSGV---RTVSVLYSGFYSLSLVTVPSSTWPSQYI-----CNVAPR---AS 88
 QY 167 NSESTQKYD---KTHNCP--PCPAPBELLGSPVLFPPKPKDTIMISRTPEVTCVVDV 220
 DB 89 KTELIRIEPIRPKPSPPGSSCPGNILGSPVFIIPPCKDMLMISTLPKVTCCVVDV 148


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OY 221 SHEDPEVFNMYVDGEVYHNATKPREBOYNSTYRVSVLTVLHODMLNGEKYKCVSNK 280
DB 149 SEDDDPVHVSWEFDNKEVHTAWTQPREAOYNSTFRVVSALPIOHODMWRKEFKCVNNK 208
OY 281 ALPAPIEKITSKAGOPREOVYTLPPSRDELTKNOVSLTCLVKGFPSPDAVEMSNCG 340
DB 209 ALPAPIERISKPKAGOPPOVYTLPPRQOMSKKVSILCTVNTFSEALSTVEMERNGE 268
OY 341 PENNYKTPPVLDSDGSFLLYSKLVTKDSKMOGNNVSCSVMEHALNHNHTQSLSPG 400
DB 269 LBDYKNTPEILDSDGYFLYSKLVTDSDWLOGEIFTCVSVMEHALNHNHTQSLSPG 328

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RESULT 8

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GCB_RAT      STANDARD:      PRT:      333 AA.
ID GCB_RAT      220761;
AC 01-FEB-1991 (rel. 17, Created)
DT 01-FEB-1991 (rel. 17, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
IG GAMMA-2B CHAIN C REGION.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
OC SEQUENCE FROM N.A.
RX MEDLINE: 89232738.
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0018; PS0018.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER      1
FT DISULFID      15
FT DISULFID      27
FT DISULFID      106
FT DISULFID      109
FT DISULFID      112
FT DISULFID      115
FT DISULFID      147
FT DISULFID      253
FT DISULFID      311
FT DISULFID      333
SQ SEQUENCE      333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

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Query Match

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Best Local Similarity 37.6%; Score 843; DB 1; Length 333;
Matches 161; Conservative 38; Mismatches 53; Indels 34; Gaps 4;

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OY 130 SNETSSKAPCRHNTGCVFGLLTOKGNATHDNICGNSSESTOKVDKT-----HTC 180
DB 66 SSVTSSTWSPQVYT-CNV-----AHASSSTKVDKVEERRNGSIGHC 106
OY 181 P-----PCPAPELLGSPVFLPPKPKDTLMISRPETCVVYVDSHEDPEVFNMYVD 234
DB 107 PCPCPTCHKCPVPELLGSPVFLPPKPKDILLISONAKYTCVAVDVSEEDPDQFSMEVN 166
OY 235 GVEVHNATKPREBOYNSTYRVSVLTVLHODMLNGEKYKCVSNKALPAPIEKITSKAK 294
DB 167 GNEVHTAQTQPREBOYNSTFRVVSALPIOHODMWSGKEFKCVNNALSPLEKITSKPK 226
OY 295 GNPREFOVYTLPPSRDELTKNOVSLTCLVKGFPSPDAVEMSNCGPENNYKTPPVLD 354
DB 227 GLVARKQVYVWGPPTQLDEQVYSLCLNSGFLPNDIGVEMTNSNGIENKNTKTEVYVMS 286
OY 355 DGSFLLYSKLVTKDSKMOGNNVSCSVMEHALNHNHTQSLSPG 400
DB 287 DGSFLLYSKLVTKDSKMOGNNVSCSVMEHALNHNHTQSLSPG 332

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RESULT 9
GCB_MOUSE     STANDARD:      PRT:      398 AA.
ID GCB_MOUSE     P03987;
AC 23-OCT-1986 (rel. 02, Created)
DT 01-AUG-1991 (rel. 19, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 85027161.
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine Ig3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
[2]
RX SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE: 84041483.
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).

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DR EMBL: J00451; AAB59655.1; -.
DR EMBL: V01526; CAA24767.1; ALT_SEQ.
DR PIR: A02155; G3MSM.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER      1
FT DOMAIN      1
FT DOMAIN      97
FT DOMAIN      98
FT DOMAIN      113
FT DOMAIN      114
FT DOMAIN      223
FT DOMAIN      224
FT TRANSMEM      346
FT TRANSMEM      363
FT TRANSMEM      368
FT TRANSMEM      398
FT TRANSMEM      399
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FT TRANSMEM      495
FT TRANSMEM      496
FT TRANSMEM      497
FT TRANSMEM      498
FT TRANSMEM      499
FT TRANSMEM      500

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Query Match

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Best Local Similarity 37.6%; Score 841.5; DB 1; Length 398;
Matches 161; Conservative 47; Mismatches 72; Indels 19; Gaps 5;

```

```

OY 107 FGVOAGIPERTVTCRCPDGFSSNETSSKAPCRHNTGCVFGLLTOKGNATHDNICSG 166
DB 42 YGALSSGV---RTVSSVLOSGEYSLSLVTVYPSSTWSPQVYT-----CNVAPR---AS 88
OY 167 NSESTOKVD---KTHTCP--PCPAPELLGSPVFLPPKPKDTLMISRPETCVVYVDSHED 220
DB 89 KTELKREIETPRKSTPPTGSSCPGNTILGSPVIFPPKPKDALLMISLTKVTCVAVDV 148
OY 221 SHEDPEVFNMYVDGEVYHNATKPREBOYNSTYRVSVLTVLHODMLNGEKYKCVSNK 280
DB 149 SEDDDPVHVSWEFDNKEVHTAWTQPREAOYNSTFRVVSALPIOHODMWRKEFKCVNNK 208

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QY 281 ALPAPIETKISKAKGPREPOVYTLPPSRDELTKNOVSLCIYKGFPSDIAVWESNGQ 340
DB 209 ALPAPIETKISKAKGPREPOVYTLPPSRDELTKNOVSLCIYKGFPSDIAVWESNGE 268
QY 341 PENNYKTPPVLDSGSEFFLYSKLTVDKSRMOQGVSCSVMEALHHYOKSLSPG 399
DB 269 LEQDYKNTPIILSDGTYFLYSLKTLVDTDSWLGSEIFTCVSHALHHHTOKLNSP 327

RESULT 10
GCL_MOUSE STANDARD: PRT: 324 AA.
ID GCL_MOUSE
AC P01868:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 80045036.
RA Horio T., Obara M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
[2]
RN SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE: 80202559.
RA Obara M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
[3]
RN SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE: 80012837.
RA Rogers J., Clarke P., Salsner W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
[4]
RN SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE: 78242288.
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma1 chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
[5]
RN DISULFIDE BONDS (MOPC 21).
RX MEDLINE: 73008889.
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
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CC
CC EMBL: V00793; CAA24172.1; -
CC EMBL: V00793; CAA24173.1; -
CC EMBL: V00793; CAA24174.1; -
CC EMBL: V00793; CAA24175.1; -
CC EMBL: V00795; CAA24176.1; -
CC PIR: A02159; GIMS.
CC MGD: MGI:96446; IGH-4.
CC INTERPRO: IPR000495; -

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DR INTERPRO: IPR003006; -.
DR PRAM: PR00047; 19; 3.
DR PROSITE: PS00290; IG_MHC. 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLUCNA. . .).
FT DISULFID 244 302
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1FC93 CRC64;

Query Match 36.6%; Score 820; DB 1; Length 324;
Best Local Similarity 60.5%; Pred. No. 6; 9e-49;
Matches 144; Conservative 45; Mismatches 39; Indels 10; Gaps 3;

QY 170 STQKVDKTHT-----CPP--CPAPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSH 222
DB 89 SSTKVKRKIVPRDCKGCKPCICIVPEV---SVYIFPKPKPDVLTITLTPKTCVVDISK 145
QY 223 EDEYKFNMYVDQVEVHNKTRREOYNSTRVYVSVLTVTHODMNGKRYKCKVSNKL 282
DB 146 DDEYQSFNFVDVEVHTAQTPREDFNSTRVYVSELPIHODMNGKFKCKVSAAP 205
QY 283 PAPIETKISKAKGPREPOVYTLPPSRDELTKNOVSLCIYKGFPSDIAVWESNGQPE 342
DB 206 PAPIETKISKAKGPREPOVYTLPPSRDELTKNOVSLCIYKGFPSDIAVWESNGE 265
QY 343 NNYKTPPVLDSGSEFFLYSKLTVDKSRMOQGVSCSVMEALHHYOKSLSPG 400
DB 266 ENYKNTPIILSDGTYFLYSLKTLVDTDSWLGSEIFTCVSHALHHHTOKLNSP 323

RESULT 11
GCL_RAT STANDARD: PRT: 326 AA.
ID GCL_RAT
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 89232738.
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0017; PS0017.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC. 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.

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P01863;
 AC 21-JUL-1986 (Rel. 01, Last Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IG GAMMA-2A CHAIN C REGION, A ALLELE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 81076554.
 RA Skorav J.-L., Auffray C., Rougeon F.;
 RT "Structure of the constant and 3' untranslated regions of the murine
 Balb/c gamma 2a heavy chain messenger RNA.";
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 81198976.
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 and evolution of heavy chain genes: further evidence for intervening
 sequence-mediated domain transfer.";
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 81223894.
 RA Ojio R., Auffray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 suggests that exons can be exchanged between genes in a multigenic
 family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RX MEDLINE: 74175517.
 RA Bourgois A., Fougereau M., Rocca-Serra J.;
 RT "Determination of the primary structure of a mouse IgG2a
 immunoglobulin: amino-acid sequence of the FC fragment. Implications
 for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435(1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE: 73056887.
 RA de Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma 2a
 immunoglobulin. Identification of the disulfide bridges.";
 RL Eur. J. Biochem. 30:452-462(1972).
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 CC EMBL: V00798; CAA24178.1; -
 DR PIR: A02152; G2MSA.
 DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DISULFID 15
 FT DISULFID 27
 FT DISULFID 107
 FT DISULFID 110
 FT DISULFID 112
 FT DISULFID 144
 FT DISULFID 250
 FT MOD_RES 330
 FT SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CRC64;
 REMOVED POST-TRANSLATIONALLY.
 INTERCHAIN (WITH A LIGHT CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).

Query Match 36.3%; Score 812.5; DB 1; Length 330;
 Best Local Similarity 56.5%; Pred No. 2,3e-48;
 Matches 137; Conservative 34; Mismatches 58; Indels 29; Gaps 4;
 QY 133 TSSKAPCRKHTNCSVFGILLTKGNATHDNCISGSESTOKYDK-----THTCPP--182
 DB 71 TSSWTFPSQISIT-CNV-----AHPASTKVKKIKIEPRGPTIKPCPPK 111
 QY 183 CPAPELLGGSPVFLFPKPKDTLMISTPEVTCVVDVSHEDPEVKNVVDQVEVNAK 242
 DB 112 CPAPNLLGGSPVFLFPKPKIDVLMISLPIVTCVVDVSDDDVDQISWNNVEVHTAQ 171
 QY 243 TKPEEDQNSTYRVSVLTFLHODWLNGKEYKGVSKALPAPIEKTIISKAKGQPREPV 302
 DB 172 TQTHREDYNTLRVVSALPFIQHODWMSGKFEKGVKNNKDPAPIERISIKPKGSVAPQV 231
 QY 303 YLPPSHDELTKNOVSLTCLVKGFPSPDAVEMESNGQPENNYKTPPVLDSDGSEFFLYS 362
 DB 232 YLPPPEEETKQVTLTQVTFDMPEDIYVETWNTNGKTELAKNTEPVLDSDGSYFMY 291
 QY 363 KLYDKRMQOGNVFSGSVNHEALNHYITOKSLSPG 400
 DB 292 KLYEKKRWERNRNSYSCSVYHEGLHNHTTKSPSRTPG 329
 RESULT 14
 GCAM_MOUSE STANDARD; PRT; 399 AA.
 ID GCAM_MOUSE
 AC P01863;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 82222190.
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 SEGMENT OF MU CHAINS.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
 IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
 THE A ALLELE.
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 CC EMBL: J00471; AAB59661.1; ALT_INIT.
 DR PIR: A02154; G2MSAM.
 DR MGD: MGI:96443; IGH-1.
 DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 Transmembrane; Alternative splicing.
 FT NON_TER 1
 FT DISULFID 15
 FT DISULFID 15
 INTERCHAIN (WITH A LIGHT CHAIN).

| | | | | | |
|----|----------|---------|-----------|--|--------------------------------------|
| FT | DISULFID | 27 | 82 | | |
| FT | DISULFID | 107 | 107 | | INTERCHAIN (WITH A HEAVY CHAIN). |
| FT | DISULFID | 110 | 110 | | INTERCHAIN (WITH A HEAVY CHAIN). |
| FT | DISULFID | 112 | 112 | | INTERCHAIN (WITH A HEAVY CHAIN). |
| FT | DISULFID | 144 | 204 | | |
| FT | DISULFID | 250 | 308 | | |
| FT | TRANSMEM | 346 | 363 | | POTENTIAL. |
| FT | DOMAIN | 364 | 399 | | CYTOPLASMIC (POTENTIAL). |
| FT | CARBOHYD | 180 | 180 | | N-LINKED (GLYCANC. . .) (POTENTIAL). |
| SO | SEQUENCE | 399 AA. | 44020 MW. | | 4C813B8FADFDF0 CRC64. |

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 36.3%; | Score 812.5; | DB 1; | Length 399; |
| Best Local Similarity | 56.58; | Pred. No. 2.8e-48; | | |
| Matches 157; | Conservative 34; | Mismatches 58; | Indels 29; | Gaps 4; |

[illegible]

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| | | | | |
|----|--|------------|-------------|------|
| DR | EMBL: | X07189; | CAA30169.1; | - |
| DR | PIR: | S00847; | S00847. | - |
| DR | INTERPRO: | IPRO00495; | - | - |
| DR | INTERPRO: | IPRO03006; | - | - |
| DR | PFAM: | PF00047; | 1g; | 3. |
| DR | PROSITE: | PS00290; | IG_MHC. | 1. |
| KW | immunoglobulin domain; Immunoglobulin C region | | | |
| ET | NON_ITER | 1 | 97 | CHI. |
| ET | DOMAIN | 1 | | |

| FT | DOMAIN | 98 | 113 | HINGE. |
|---|----------|---------|-----------|---------------------------------|
| FT <td>DOMAIN</td> <td>114</td> <td>222</td> <td>CH2.</td> | DOMAIN | 114 | 222 | CH2. |
| FT <td>DOMAIN</td> <td>223</td> <td>329</td> <td>CH3.</td> | DOMAIN | 223 | 329 | CH3. |
| FT <td>DISULFID</td> <td>15</td> <td>15</td> <td>INTERCHAIN (WITH A LIGHT CHAIN)</td> | DISULFID | 15 | 15 | INTERCHAIN (WITH A LIGHT CHAIN) |
| FT <td>DISULFID</td> <td>27</td> <td>82</td> <td></td> | DISULFID | 27 | 82 | |
| FT <td>DISULFID</td> <td>111</td> <td>111</td> <td>INTERCHAIN (WITH A HEAVY CHAIN)</td> | DISULFID | 111 | 111 | INTERCHAIN (WITH A HEAVY CHAIN) |
| FT <td>DISULFID</td> <td>113</td> <td>113</td> <td>INTERCHAIN (WITH A HEAVY CHAIN)</td> | DISULFID | 113 | 113 | INTERCHAIN (WITH A HEAVY CHAIN) |
| FT <td>DISULFID</td> <td>143</td> <td>203</td> <td></td> | DISULFID | 143 | 203 | |
| FT <td>DISULFID</td> <td>249</td> <td>307</td> <td></td> | DISULFID | 249 | 307 | |
| SO <td>SEQUENCE</td> <td>329 AA;</td> <td>35571 MM;</td> <td>5FCD7B7933850773 CRC64;</td> | SEQUENCE | 329 AA; | 35571 MM; | 5FCD7B7933850773 CRC64; |

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 35.9% | Score 804.5; | DB 1; | Length 329; |
| Best Local Similarity | 63.7% | Pred. No. 7.9e-48; | | |
| Matches 142; | Conservative 41; | Mismatches 37; | Indels 3; | Gaps 1. |

| | | | |
|----|-----|--|-----|
| Qy | 181 | PP--CPAPBELLGGPSVLEFPFKKIDLMISRPEVCVVAVDSHEBPXKFNMYVQGE | 237 |
| Db | 106 | PPDLCSCDDMLGNRPSPVIFPPKFKDMLTLPILVAVCVVDSSEEDPQVQSFNFVNR | 166 |
| Qy | 238 | VHNAKTKREBOYASTRYVSVLVFLVHODVLMNGKREYKCKVSNKALPAPRIEKTISKAGOP | 297 |
| Db | 166 | VETAGTQGHEDLNGTFRVAVSTLIHQHODMMKSGREFCKVYNNKRDLPSPRIEKTISKPRGA | 228 |
| Qy | 298 | REPQYVITLPPSRDELTKNQVSLJCLVKGFIPIPSDIAVEMESNGOPENNYKTTPPVLSDGS | 357 |
| Db | 226 | RTPOYVITLPPREBOMSKNKVSILCMVTSFPAISIVSEMERGELEODYKNTLPVLDDDES | 285 |
| Qy | 358 | FELYSKLTVDSKRMQOGVSCSYMHENLHHYQOKSLSPSG | 400 |
| Db | 286 | YFLYSKLSVDTSMMRGDITCSVYHNEHLNHHYQOKULSRSPG | 328 |

Search completed: December 27, 2000, 10:55:07
Job time: 209 sec.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:52:38 ; Search time 60.82 Seconds
(without alignments)
614.102 Million cell updates/sec

Title: US-09-389-545-5

Perfect score: 2240
Sequence: 1 ETTPPKYLAHDETSNQLC.....VMHEALHNHYTKSLSPG 400

Scoring table: BIOSUM62
Gap0 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP-REMBL.14:*
2: SP-archaea:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-----------|--------------------|
| 1 | 1013.5 | 45.2 | 401 | 4 000300 | 000300 homo sapien |
| 2 | 1013 | 45.2 | 372 | 4 090HP4 | 090HP4 homo sapien |
| 3 | 893.5 | 39.9 | 401 | 11 008712 | 008712 mus musculu |
| 4 | 877 | 39.2 | 401 | 11 008727 | 008727 ratus norv |
| 5 | 827 | 36.9 | 437 | 11 09R1A4 | 09R1A4 mus musculu |
| 6 | 433 | 19.3 | 300 | 4 095407 | 095407 homo sapien |
| 7 | 405.5 | 18.1 | 302 | 13 09PUS0 | 09PUS0 salvelinus |
| 8 | 345 | 15.4 | 459 | 11 062327 | 062327 mus musculu |
| 9 | 343.5 | 15.3 | 439 | 4 016042 | 016042 homo sapien |
| 10 | 338 | 15.1 | 482 | 11 088734 | 088734 mus musculu |
| 11 | 297 | 13.3 | 655 | 4 075509 | 075509 homo sapien |
| 12 | 280.5 | 12.5 | 684 | 13 090544 | 090544 ginsylmosto |
| 13 | 277.5 | 12.4 | 384 | 4 090P60 | 090P60 homo sapien |
| 14 | 258.5 | 11.5 | 616 | 4 091608 | 091608 homo sapien |
| 15 | 236.5 | 11.5 | 625 | 11 035305 | 035305 mus musculu |
| 16 | 241 | 10.8 | 349 | 12 057099 | 057099 monkeypox v |
| 17 | 239 | 10.7 | 349 | 12 057291 | 057291 monkeypox v |
| 18 | 239 | 10.7 | 349 | 12 057100 | 057100 monkeypox v |
| 19 | 239 | 10.7 | 349 | 12 057101 | 057101 monkeypox v |

| | | | | | |
|----|-------|------|-----|-----------|--------------------|
| 20 | 239 | 10.7 | 349 | 12 057102 | 057102 monkeypox v |
| 21 | 235.5 | 10.5 | 348 | 12 057277 | 057277 monkeypox v |
| 22 | 235.5 | 10.5 | 348 | 12 057103 | 057103 monkeypox v |
| 23 | 235.5 | 10.5 | 348 | 12 057108 | 057108 monkeypox v |
| 24 | 229 | 10.2 | 348 | 12 057112 | 057112 variola vir |
| 25 | 229 | 10.2 | 348 | 12 085407 | 085407 variola vir |
| 26 | 226.5 | 10.1 | 349 | 12 057284 | 057284 variola vir |
| 27 | 226.5 | 10.1 | 349 | 12 057098 | 057098 variola vir |
| 28 | 226 | 10.1 | 349 | 12 057110 | 057110 variola vir |
| 29 | 226 | 10.1 | 349 | 12 057111 | 057111 variola vir |
| 30 | 226 | 10.1 | 349 | 12 089098 | 089098 variola vir |
| 31 | 226 | 10.1 | 349 | 12 089098 | 089098 variola vir |
| 32 | 223 | 10.0 | 350 | 12 057115 | 057115 variola vir |
| 33 | 222.5 | 9.9 | 349 | 12 057097 | 057097 variola vir |
| 34 | 222.5 | 9.9 | 350 | 12 057123 | 057123 variola vir |
| 35 | 222.5 | 9.9 | 355 | 12 085308 | 085308 variola vir |
| 36 | 221 | 9.9 | 349 | 12 057109 | 057109 variola vir |
| 37 | 220.5 | 9.8 | 349 | 12 057305 | 057305 variola vir |
| 38 | 219 | 9.8 | 326 | 12 057122 | 057122 variola vir |
| 39 | 218.5 | 9.8 | 360 | 12 057118 | 057118 variola vir |
| 40 | 217.5 | 9.7 | 326 | 12 057120 | 057120 variola vir |
| 41 | 217.5 | 9.7 | 351 | 12 073559 | 073559 variola vir |
| 42 | 216.5 | 9.7 | 351 | 12 057117 | 057117 variola vir |
| 43 | 212.5 | 9.5 | 347 | 12 057115 | 057115 variola vir |
| 44 | 210.5 | 9.4 | 316 | 12 057092 | 057092 variola vir |
| 45 | 210.5 | 9.4 | 320 | 12 057300 | 057300 variola vir |

ALIGNMENTS

| RESULT | ID | SEQUENCE | PRELIMINARY | PRT | 401 AA. |
|--------|--|---|-------------|-----|---------|
| 000300 | 000300 | 000300; 060236; | | | |
| AC | 01-JUL-1997 | (TREMBLrel. 04, Created) | | | |
| DT | 01-JUL-1997 | (TREMBLrel. 04, last sequence update) | | | |
| DT | 01-MAY-2000 | (TREMBLrel. 13, last annotation update) | | | |
| DE | OSTEOCALCIN PRECURSOR (OSTEOCALCINOGENESIS INHIBITORY FACTOR) | | | | |
| DE | (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B). | | | | |
| GN | TNFRSF11B OR OPG OR OCIF. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| RN | [1] | SEQUENCE FROM N.A. | | | |
| RP | TISSUE=KIDNEY. | | | | |
| RC | MEDLINE: 97262071. | | | | |
| RA | Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., | | | | |
| RA | Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., | | | | |
| RA | Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., | | | | |
| RA | Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., | | | | |
| RA | Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., | | | | |
| RA | Suags S., Boyle W.J.; | | | | |
| RT | "Osteoprotegerin: a novel secreted protein involved in the regulation | | | | |
| RT | of bone density." | | | | |
| RL | Cell 89:309-319(1997). | | | | |
| RL | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=LUNG FIBROBLAST; | | | | |
| RA | MEDLINE: 98151033. | | | | |
| RA | Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., | | | | |
| RA | Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., | | | | |
| RA | Tsuda E., Morinaga T., Higashio K.; | | | | |
| RT | "Identity of osteocalcinoegenesis inhibitory factor (OCIF) and | | | | |
| RT | osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits | | | | |
| RT | osteoclastogenesis in vitro." | | | | |
| RL | Endocrinology 139:1329-1337(1998). | | | | |
| RL | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=PLACENTA; | | | | |
| RA | MEDLINE: 98351569. | | | | |
| RA | Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.; | | | | |

Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor;
 Eur. J. Biochem. 254:685-691(1998).
 -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AB002146; BAA25910.1; -
 DR EMBL: AB008822; BAA32076.1; -
 DR EMBL: AB008821; BAA32076.1; JOINED.
 DR EMBL: U94332; AAB53709.1; -
 DR HSSP: P25942; ICDF.
 DR MIM: 602643; -
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KM Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 183 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 152 152 POTENTIAL.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
 SQ SEQUENCE 401 AA; 4596 MW; EB42FA51C9D7C71E CRC64;

Query Match 45.2%; Score 1013.5; DB 4; Length 401;
 Best Local Similarity 68.7%; Pred. No. 4.5e-81;
 Matches 193; Conservative 12; Mismatches 37; Indels 39; Gaps 5;

QY 1 ETPPPKYLHDEETSHQLCDKCPGGTYLKQCTAKWKYCAPCPDHYTDSWHTSDECL 60
 DB 22 ETPPPKYLHDEETSHQLCDKCPGGTYLKQCTAKWKYCAPCPDHYTDSWHTSDECL 81
 QY 61 YCSVPCKELOYVQECNRTNRYCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPRNTV 120
 DB 82 YCSVPCKELOYVQECNRTNRYCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPRNTV 141
 QY 121 CKRCPDGFFSNETSAPKCRKHTNCSVFGLLLQKGNATHDNICSGNSESTOKVXTHTC 180
 DB 142 CKRCPDGFFSNETSAPKCRKHTNCSVFGLLLQKGNATHDNICSGNSESTOKVXTHTC 194
 QY 181 PCPCAPPELLGSPVFLPPPKDITMISRPDYTCVVDVSHEDPEYKFNMYDGVGVHN 240
 DB 195 --CGIDVTLCEEAFFRAVPATK-----FTPNMLSVLD-----NLPGTRVNA 234
 QY 241 AKTKPREQYNSYRVSVTLVHQLDNLNGKEYCKYSNKA 281

DB 235. ESVERIKRQSSQEQTFOLKL-----KHQNK 263

RESULT 2
 ID 09HP4 PRELIMINARY; PRT; 372 AA.
 AC 09HP4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE OSTEOPROTEGERIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
 RT "Cloning and Expression of Osteoprotegerin from Homo sapiens."
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
 DR EMBL: AF134187; AAF20168.1; -
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 FT NON_TER 1
 SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CDD3 CRC64;

Query Match 45.2%; Score 1013; DB 4; Length 372;
 Best Local Similarity 73.4%; Pred. No. 4.5e-81;
 Matches 190; Conservative 10; Mismatches 35; Indels 24; Gaps 5;

QY 1 ETPPPKYLHDEETSHQLCDKCPGGTYLKQCTAKWKYCAPCPDHYTDSWHTSDECL 60
 DB 1 ETPPPKYLHDEETSHQLCDKCPGGTYLKQCTAKWKYCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSVPCKELOYVQECNRTNRYCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPRNTV 120
 DB 61 YCSVPCKELOYVQECNRTNRYCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPRNTV 120
 QY 121 CKRCPDGFFSNETSAPKCRKHTNCSVFGLLLQKGNATHDNICSGNSESTOKVXTHTC 180
 DB 121 CKRCPDGFFSNETSAPKCRKHTNCSVFGLLLQKGNATHDNICSGNSESTOKVXTHTC 173
 QY 181 PCPCAPPELLGSPVFLPPPKDITMISRPDYTCVVDVSHEDPEYKFNMYDGVGVHN 240
 DB 174 --CGIDVTLCEEAFFRAVPATK-----FTPNMLSVLD-----NLPGTRVNA 217
 QY 241 AKTKPREQYNSYRVSV 259
 DB 218 -RIKQHSQEQTFOLKL 235

RESULT 3
 ID 008712 PRELIMINARY; PRT; 401 AA.
 AC 008712; 070202;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF).
 GN TNFRSF11B OR OPG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-KIDNEY;
 RX MEDLINE; 97262071.
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,

| FT | VARIANT | 296 | 296 | L -> R (IN STRAINS 129/OLA AND NIH SWISS). |
|--------|---|---|-----------|--|
| FT | SEQUENCE | 401 AA: | 45923 MW: | CAA6102DB312470 CRC64: |
| QY | 1 | ETFPFKLHDEETSHQGLCDKCPPEGYTLKQKSTAKMKYVACAPCPDHYTDSMHTSDECL | 60 | |
| QY | 22 | ETLPFKLHADPEHGQGLCDKCAPGYTLKQKSTAKMKYVACAPCPDHYTDSMHTSDECV | 81 | |
| QY | 61 | YCSVCKELOYVQEOECRTNRCVCEKREGRYLEIEFCLKHSRCPFGVQAGTEPRNTV | 120 | |
| QY | 82 | YCSVCKELOYVQEOECRTNRCVCEKREGRYLEIEFCLKHSRCPFGVQAGTEPRNTV | 141 | |
| QY | 121 | CKRCPDGFSNETSKAPCKRHTNSVFGLLTLQKGNATHDNICSGNSESTOKVDKHTC | 180 | |
| QY | 142 | CKRCPDGFSNETSKAPCKRHTNSVFGLLTLQKGNATHDNICSGNSESTOKVDKHTC | 194 | |
| QY | 181 | PCGAPRLGSPVFLFPKPKNTLMISRPVTCVYVDVSHEDPEYKKNVYDVEYHN | 240 | |
| QY | 195 | -CGIDVTLCEEAFFRPAFTK-----IIPMLSVLV- --SLPQKVN--AESVE-- | 238 | |
| QY | 241 | AKTPREQYNSYRVVSVLTVDHOMLNGEY-----RCKYS----- | 278 | |
| QY | 239 | RIRRRSSQEQFOLLKMKHNRQEWKTLIDIDCESSYGRHLGNSMLTTEQLLA | 297 | |
| QY | 279 | -----NKALPAPLEIKTSKAGQPREPOVYTL---PSSDELTKNOVSLTCLYKGFY | 327 | |
| QY | 298 | LMESLPKKTSPSEIERTRKTSKSQLKLTLMLRKINGDDTLGLMYALKHKTSHF | 357 | |
| QY | 328 | PSDIAYEMSGOPENNYKTPVLDSDSFFLYSLTYD | 367 | |
| QY | 358 | PKTYT-----HSKRKTMTFLHSFTMYRLYQKLFDE | 387 | |
| RESULT | 4 | | | |
| 008727 | | PRELIMINARY; | PRT; | 401 AA. |
| AC | 008727 | | | |
| DT | 01-JUL-1997 (TEMBLrel. 04, Created) | | | |
| DT | 01-JUL-1997 (TEMBLrel. 04, Last sequence update) | | | |
| DT | 01-MAY-2000 (TEMBLrel. 13, Last annotation update) | | | |
| DE | OSTEOBROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) | | | |
| DE | (OICP) | | | |
| GN | TNRSFLIB OR OPG. | | | |
| OS | Rattus norvegicus (Rat). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=INTESTINE; | | | |
| XX | MEDLINE: 97262071. | | | |
| RA | Stimomet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., | | | |
| RA | Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., | | | |
| RA | Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., | | | |
| RA | Baevy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., | | | |
| RA | Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., | | | |
| RA | Suggs S., Boyle W.J., | | | |
| RT | *osteoprotegerin: a novel secreted protein involved in the regulation | | | |
| RT | of bone density." | | | |
| RL | Cell 89:309-319(1997). | | | |
| CC | -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES | | | |
| CC | OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY | | | |
| CC | SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO | | | |
| CC | OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN | | | |
| CC | STROMAL CELLS AND OSTEOCLAST PROGENITORS. | | | |
| CC | -1- SUBUNIT. HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY | | | |
| CC | SIMILARITY). | | | |
| CC | -1- SUBCELLULAR LOCATION: EXTRACELLULAR. | | | |
| CC | -1- SIMILARITY. CONTAINS A LA-NGF/TNFR-TYPE CYSTEINE-RICH REGION. | | | |

DR EMBL: U94330; AAB53707.1; -
 DR HSSP: P25942; ICDF
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 2.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 201 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT SEQUENCE 401 AA; 46192 MW; FEC6A31F1DAE573A CRC64;

Query Match 39.2%; Score 877; DB 11; Length 401;
 Best Local Similarity 63.7%; Pred. No. 4.2e-69;
 Matches 165; Conservative 18; Mismatches 52; Indels 24; Gaps 5;

QY 1 ETPPKYIHYBEERSHOLCDKCPGTYLKQCTAKMTVCAPCDHYTDSMHTSDCL 60
 DB 22 ETPPKYIHYBEERSHOLCDKCPGTYLKQCTAKMTVCAPCDHYTDSMHTSDCL 81
 QY 61 YCSPYCKELQYVOCENRHNVCCECKRGYLEIEFCCKHSCPGFGVVOAGPERMTY 120
 DB 82 YCSPYCKELQYVOCENRHNVCCECKRGYLEIEFCCKHSCPGFGVVOAGPERMTY 141
 QY 121 CKRCPDGFSSNETSKACRKHNTCSVGLLLTQGNATHDNICGNSGSESTQKYDKHTC 180
 DB 142 CKRCPDGFSSNETSKACRKHNTCSVGLLLTQGNATHDNICGNSGSESTQKYDKHTC 194
 QY 181 PRCAPBELGSPVFLPPKPKDITMISRTPEYCVVVDVSHEDPEVFNMTYDGEVHN 240
 DB 195 --CGIDVTLCGEAFREAVPTR-----TIPNWLSLVD---SLPGTYN--AESVE--- 238
 QY 241 AKTRPREQYNTYRVVSV 259
 DB 239 -RIKRHSSQEQTFOLKL 256

RESULT 5
 Q9RIA4 PRELIMINARY; PRT; 437 AA.
 ID Q9RIA4
 AC Q9RIA4
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.C., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFv).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF152372; AAD40243.1; -

DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; IG; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 437 437
 FT SEQUENCE 437 AA; 48142 MW; 5C3A7B33EE7D697C CRC64;

Query Match 36.9%; Score 827; DB 11; Length 437;
 Best Local Similarity 60.9%; Pred. No. 1.1e-64;
 Matches 145; Conservative 44; Mismatches 39; Indels 10; Gaps 3;

QY 170 STQVVDKHT-----CPR--CPABELLGSPVFLPPKPKDITMISRTPEYCVVVDVSH 222
 DB 202 STQVVDKHT-----CPR--CPABELLGSPVFLPPKPKDITMISRTPEYCVVVDVSH 258
 QY 223 EDPEVKFMVYDGEVHNACTRPREQYNTYRVVSVTLVLDHODLNGKCKRYSKAL 282
 DB 259 DDPEVQFMVYDGEVHNACTRPREQYNTYRVVSVTLVLDHODLNGKCKRYSKAL 318
 QY 283 PAPLEKITSKAKGPREPOVYTLPPSRDELTKNOVSLTCLYKGFPSDIAVWESNGOPE 342
 DB 319 PAPLEKITSKAKGPREPOVYTLPPSRDELTKNOVSLTCLYKGFPSDIAVWESNGOPE 378
 QY 343 NNYKTPVLDSGSPFLYSKLTVDKSMOOGNVFSGSVHMEALHNHYTKSLSPG 400
 DB 379 ENYKTPVLDSGSPFLYSKLTVDKSMOOGNVFSGSVHMEALHNHYTKSLSPG 436

RESULT 6
 Q95407 PRELIMINARY; PRT; 300 AA.
 ID Q95407
 AC Q95407
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE DECOY RECEPTOR 3.
 GN DCR3 OR TR6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 99087326.
 RA Pitti R.M., Maisters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
 RA Goddard A.D., Botstein D., Ashkenazi A.;
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RT colon cancer";
 RL Nature 396:699-703(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE: 99253915.
 RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 RT "A newly identified member of tumor necrosis factor receptor
 RT superfamily (TR6) suppresses LIGHT-mediated apoptosis";
 RL J. Biol. Chem. 274:13733-13736(1999).
 DR EMBL: AF104419; AAD03056.1; -
 DR EMBL: AF134240; AAD29688.1; -
 DR HSSP: P25942; ICDF
 DR INTERPRO: IPR000561; -
 DR INTERPRO: IPR001366; -
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 2.
 KW Receptor.
 SO SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;

| | |
|---------------------------|--|
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-NOD; |
| RX | MEDLINE; 95178848. |
| RA | Powell E.E., Micker L.S., Peterson L.B., Todd J.A.; |
| RT | "Allelic variation of the type 2 tumor necrosis factor receptor gene." |
| RL | Mamm. Genome 5:726-727(1994). |
| DR | EMBL; X76401; CAAS3981.1; - |
| DR | HSSP; P19438; INCF. |
| DR | INTERPRO; IPR001368; - |
| DR | PFAM; PF00020; TNFR_C6_4 |
| DR | PROSITE; PS00652; TNFR_NGFR.1; 2. |
| DR | PROSITE; PS00500; TNFR_NGFR.2; 3. |
| FT | NON_TER |
| FT | VARIANT |
| FT | VARIANT |
| FT | VARIANT |
| FT | VARIANT |
| FT | VARIANT |
| SO | SEQUENCE |
| Query Match | 15.4%; Score 345; DB 11; Length 459; |
| Best Local Similarity | 25.2%; Pred. No. 2,2e+22; |
| Matches 100; Conservative | 53; Mismatches 164; Indels 80; Gaps 12. |
| OY | 9 HYDETSHQLLCDRCPTGYLKHCTAKTKVCAAPCPDHYTDSWHTSDECLYCSPVCKE 68 |
| Dd | 31 YIDKRA--QMCACACPPGOYVHKHCNKTSIDVICADCEASMTYGVNQFRTGLSCSSCST 88 |
| OY | 59 LQYKQECNRTHNYRVECKEGRYLEIEF-----CLKHRSCEPGFYVQAQTPERNIVC 121 |
| Dd | 89 DQVETFACTKOONRKACACEAGRYCALKTSHSGSCROCMRLSKCGPEFGVAASSRAPNGNYLC 148 |
| OY | 122 KRCRDGEFSNNTSSAPCRKHTNCSVFELLTLQGNATHDNICSNSTQKV-----174 |
| Dd | 149 KACACGTSDTSTSDVCVRPHRICSLAI---PQNASITDACAPESPTLSAIPRTLYVS 204 |
| OY | 175 --DKHTCP-----PCPAPELL-----GGPSV-----FLFPKK 200 |
| Dd | 205 QEPETRPDLQEPGPSOTPSILTSLGSTPIIESTKGISLTPLIGLYGYSGLMLGL 264 |
| OY | 201 PKDTLMISRTEPVTCVVVDVSHEDPEVKFNMYVDGVEVHNAAKTRPREOYNSTRYAVSVL 260 |
| Dd | 265 VNCFTLVQRKKPKSLQIDA--KVPHVDEKSQDAVL-----EQOH-----LL 306 |
| OY | 261 TVLRHDWLNGEKYEKCYSNKAALPA---PLEKITSIAKQOPREPQYTLPSPDELTKNOY 317 |
| Dd | 307 TTAASSSSSSLESSASAGDRAPPGHGHOARMEAOGSQEARASSRISDSHSGHGTNV 366 |
| OY | 318 SLTCLVKGFYPSDIAEVESN----GQPENNYKTT 349 |
| Dd | 367 NVTCIVNCCSSDHSSQCSSQASATVGDPDAKPASP 403 |
| RESULT | 9 |
| ID | 016042 PRELIMINARY; PRT: 439 AA. |
| AC | 016042; |
| DT | 01-NOV-1996 (TREMBLrel. 01, Created) |
| DT | 01-JAN-1999 (TREMBLrel. 09, Last sequence update) |
| DT | 01-MAY-2000 (TREMBLrel. 13, Last annotation update) |
| OS | TUMOR NECROSIS FACTOR RECEPTOR. |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE; 91370690. |
| RA | Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R., Brockhaus M., Lesslauer W.; |


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Db 54 YRHADRATGQVLACDKCPACTYVSEHCNTSLRYCSCSPVGTFRHNGIEKHCDSQPC 113
QY 67 KEIQYKQECNKRHNRYCEKEGRHYLEIFCLKHSRCPGEGVYQACTPERANTYCKACPD 126
Db 114 PWDMEIKELPCALDLRECTCPGPGFQSNATCAPHTVCPVGMGYKAKKSTEDVYCKOCAR 173
QY 127 GPFNSNERSAPCRKHNCVSGFLLLOKGNATHDNICS--GNSESTQVADKHTHTPPC 183
Db 174 GTSIDVPSSWMCKAYDCLDSQNLVYIKPGKRTDNVCGTLPSFSSSTS----- 222
QY 184 PABELLGGPSEVFLPPPKRDTLMISRTPEYTCVYVDVSHED-----PEVKFNMYVDG 235
Db 223 PSP-----GTAIF--PRP-EHMEHVEPSSTYPKGNMSTESNSASVRRKV-LSSIQEG 273
QY 236 VEYHNAKTRPREQYNTYVSVLVHODWLNKGEYCKCKVSKNALPAP1---EKTIS 291
Db 274 TVPDNTSSAGKEDVYNT--LPNLQVYVNHQ---QGPHRHL--KLPSMEATGGEKST 326
QY 292 KAKGPR 298
Db 327 PIRPKR 333

RESULT 12
ID 090544 PRELIMINARY: PRT: 684 AA.
AC 090544;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE NOVEL ANTIGEN RECEPTOR PRECURSOR.
OS Ginglymostoma citratum (Nurse Shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
OC Orectolobiformes; Ginglymostomidae; Ginglymostoma.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-SPLEN;
RC MEDLINE: 95183140.
RX Greenberg A.S., Avila D., Hughes M., McKlincy E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).
EMBL: U18701; AAB48195.1; -.
DR INTERPRO: IPR003006; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 6.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
DR Signal.
RT SIGNAL.
RT CHAIN 1 18 POTENTIAL.
RT SEQUENCE 684 AA: 75224 MW: 2FF9D2071CDA6DFD CRC64;

Query Match 12.5%; Score 280.5; DB 13; Length 684;
Best Local Similarity 26.5%; Pred. No. 1.6e-16;
Matches 103; Conservative 53; Mismatches 148; Indels 85; Gaps 18;
QY 51 DSWHTSDECIYCS-----PVCKELQYKQECNKRHNRYCEKEGRHYLEIFCLKHSR 102
Db 315 EWMOSGGE-YTCAKAKQOSSTPYKRRKARVETKPHML----- 354
QY 103 CPGGFGVQAQTPRNTVYKCRPDGFFSNETS--SKAPCRKHTNCSVFGLLLTQ----- 154
Db 355 LPSPPEIIOGTSATLCLIR--GFYPRKYVSWQKDVSVSANTYNTFPALEODLTF 411
QY 155 -----KGNATHNICGN-----SEST-----QKVDKTHICPPCAPELLGPR 192
Db 412 TRSLNLTAVEMSGAKY--TCTASHPPSOSTYKRVIRNOKVD-----CRQTDI---- 458
QY 193 SVFLFPPKPDITMISRTPEYTCVYVDVSHEDPE-VKFNMYVDGVEYHNAKTRPREQYN 251

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Db 459 SVSLKRP-PEELIMTQOTATVCEIY---YSDLENIKVEMQVNGVERKKGVETQNPWMSG 514
QY 252 STRVSVSVTLVHODWLNKGEYCKCKVSKNALPAPIEKTSKAK-GORPREQVYTLPPSRD 310
Db 515 SKSTIVSKLVMASEWDSGTEYVCLVEDSELPTPVKASIRKANVSOMHPKRYLLHPSTD 574
QY 311 EL-TKNQVSLTCLVKGYPYSDIYVEMESNGQ-PENNYKTTPLVLDSDGSEFLSKLTVDK 368
Db 575 EIDTESATIMCLATNHPAELIYGMWANDTLDSGRTQVDSEKSGSEFVDRLLTA 634
QY 369 SRMOQGVFSCSVMEALHN--HYTOKS 394
Db 635 AEMNSDTTYSCLVGHPSLNDLIRSTINKS 663

RESULT 13
ID 09060 PRELIMINARY: PRT: 384 AA.
AC 09060;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE SNC73 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RP Zheng S., Cao J., Cao W., Cai X., Geng L.;
RT "Identification and characterization of SNC73, a gene which is down-
RT regulated in colorectal cancer.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
EMBL: AF067420; AAC19365.1; -.
DR INTERPRO: IPR003006; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
RN SEQUENCE 384 AA: 40947 MW: BAYADC3CA5A9DD48 CRC64;

Query Match 12.4%; Score 277.5; DB 4; Length 384;
Best Local Similarity 28.6%; Pred. No. 1.5e-16;
Matches 95; Conservative 35; Mismatches 141; Indels 61; Gaps 13;
QY 115 PERNTYCKRCPDGFPSNE-----TSSKAPCRKHTNCSVFGLLLTQ 155
Db 49 PDGNNVYIACLVGFFPQEPPLSVTWSESGGVTAARNPPSQDAGDLXTTSQULTPATQ- 107
QY 156 GNATHNICGSESTQKDKTICP-----PCPABELLGGSVFLFPKPR----- 202
Db 108 -----CLAGKSVYCHV-KHYTNPSQDYTPCPVPSTPPTPST-PTPSPSCCHPR 157
QY 203 -----DTLMISRTPEYTCVYVDVSHEDPEVKFNMYVDGVEYHNAKTRPREQYNSTY 254
Db 158 LSLHRALEDLLIGSEANLTCITLGE--RDASGVTFWTPTBSGR--SAYGCPRRDLGGCY 214
QY 255 RVVSVTLVHODWLNKGEYCKCKVSKNALPAPIEKTSKAKGPREQVYTLPPSRDELTK 314
Db 215 SVSSVLPVPGCAEPPNHNKTEFTCTAAYPESKTPLATLSKS-GNTPREVEHLPPPESEAL 273
QY 315 NO-VSLTCLVKGYPYSDIYVEMESNGQ--PENNYKTTPLVD--SDG--SFELSKLTVDK 368
Db 274 NELVTLTCLARGSPQDVAVLRWLQSGOELPREKYLTVWASRQPSQGTTFVAVSLVAA 353
QY 369 SRMOQGVFSCSVMEALHNHYTOKSLSPG 400
Db 334 EDWKKGDTFSCWGHALPLATQKTIIDRLAG 365

RESULT 14
ID 09Y606 PRELIMINARY: PRT: 616 AA.

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AC 09Y606:
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
DE INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF1A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98032977.
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tomelesko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
Nature 390:175-179(1997).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC GLAND.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AF018253; AAB86809.1; -
DR MIM; 603499; -
DR INTERPRO; IPR001368; -
DR PFM; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT SIGNAL 1 22
FT CHAIN 23 616
FT DOMAIN 24 212
FT TRANSSEM 213 233
FT DOMAIN 234 616
FT DOMAIN 33 195
FT REPEAT 33 69
FT REPEAT 70 112
FT REPEAT 113 152
FT REPEAT 153 195
FT DISULFID 34 46
FT DISULFID 47 60
FT DISULFID 50 68
FT DISULFID 71 86
FT DISULFID 92 112
FT DISULFID 114 124
FT DISULFID 126 133
FT DISULFID 127 151
FT DISULFID 154 169
FT DISULFID 175 194
FT CARBOHYD 105
FT CARBOHYD 174
SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;
Query Match 11.5%; Score 258.5; DB 4; Length 616;
Best Local Similarity 34.5%; Pred. No. 1.2e-14;
Matches 58; Conservative 21; Mismatches 82; Indels 7; Gaps 4;
QY 20 CDKCPPTGYLKHQHTAKWKVCAPCPDHYTDSWHTSDECLYCSPVC--KELQYVKQEC 76
DB 47 CNKCEPFGKYMSSKCTTTSDSVCLPCGPDDEYLDSDWNEEDKCL-LHAYCOTGRALVAVAG- 104
QY 77 NRTNHRVCEKEGRY--LEIEFCLKHSRCPGFGVVOAGTPERNTVCKRCPDGFFSNETS 134
DB 105 NSTPFRACAGTAGYHWSQDCECCRRNTECAPGAGHPLQLNKDTVCKPCLAGYSDAFS 164
QY 135 SKAPRKATNCSTVGLLLTQKGNATHDNICGNSSESTOKVDTHTKCP 182
DB 165 STDKRPWTNCTFLKRVENHGTESDAVCSSSLPAPRPNEPHYLLP 212
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RESULT 15
ID 035305 PRELIMINARY; PRT; 625 AA.
AC 035305
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
DE INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF1A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-LIVER EPITHELIUM;
RX MEDLINE; 98032977.
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tomelesko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
Nature 390:175-179(1997).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AF019046; AAB86810.1; -
DR HSSP; P25942; IGDF.
DR MGD; MGI:1314891; Tnfrsf1a.
DR INTERPRO; IPR001368; -
DR PFM; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT SIGNAL 1 30
FT CHAIN 31 625
FT DOMAIN 31 214
FT TRANSSEM 215 235
FT DOMAIN 236 625
FT DOMAIN 34 196
FT REPEAT 34 70
FT REPEAT 71 114
FT REPEAT 115 153
FT REPEAT 154 196
FT DISULFID 35 47
FT DISULFID 48 61
FT DISULFID 51 69
FT DISULFID 72 87
FT DISULFID 93 113
FT DISULFID 115 125
FT DISULFID 127 134
FT DISULFID 128 152
FT DISULFID 155 170
FT DISULFID 176 195
FT CARBOHYD 106
FT CARBOHYD 175
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511DBE CRC64;
Query Match 11.5%; Score 256.5; DB 11; Length 625;
Best Local Similarity 25.3%; Pred. No. 1.8e-14;
Matches 102; Conservative 41; Mismatches 147; Indels 113; Gaps 17;
QY 20 CDKCPPTGYLKHQHTAKWKVCAPCPDHYTDSWHTSDECLYCSPVC--KELQYVKQEC 76
DB 48 CSRCEPFGKYMSSKCTTTSDSVCLPCGPDDEYLDTWNEEDKCL-LHAYDAGALVAV-DPG 105
QY 77 NRTNHRVCEKEGRY--LEIEFCLKHSRCPGFGVVOAGTPERNTVCKRCPDGFFSNETS 134
DB 106 NHTAPRRACAGTAGYHWSQDCECCRRNTECAPGAGHPLQLNKDTVCTPCLAGFFSDVFS 165
```

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OY 135 SKAPCRKHTNCVSFGLLTKGNATHDNICSGNSESTQKVDKTHTCPCPAPBLGSPV 194
Db 166 STDCKPMTNCTLLGKLEAHOGTTESDVCGSS-----MTLRPRPKEAQYL--PSL 215
OY 195 FLPPPKRDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTY 254
Db 216 IVL-----LFISSVVAAILIFGV-----YRKGR----- 241
OY 255 RVSVSLTVLHODWLN-----GKEY--KCRVSNKA-----LPAPIEKTIS 291
Db 242 ----ALTANLMNWNVDACSSLSGKNKSSGDRCAGSHSATSSQOVCBGILLMTREKMP 297
OY 292 K-----AKGP-----REPOVTL-----PSRDEL--KNQVSLTCL 322
Db 298 EDGAGVCGPVCAAGPMAEYRDSRTFTLVSEVETQGDLSRKIPTEDYTDPSOPSTGSL 357
OY 323 V-----KGFYPSDIAVEMESNGOPENNYKTPPVLDSDGSFF 359
Db 358 LLIQGSKSIRPFQEPLEVGENDLSQCFGTGTESTYDSECGDF 400

```

Search completed: December 27, 2000, 10:52:40
 Job time: 71 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:51:29 ; Search time 60.82 Seconds

(without alignments)
615.637 Million cell updates/sec

Title: US-09-389-545-2

Perfect score: 2179
Sequence: 1 MNKKLCCALVLDLIEWT.....OKLFLEMIGNQSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 297973

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------------|
| 1 | 2179 | 100.0 | 401 | 11 | 008712 mus musculu |
| 2 | 2079 | 95.4 | 401 | 11 | 008727 rattus norv |
| 3 | 1892 | 86.8 | 401 | 4 | 000300 homo sapien |
| 4 | 1789 | 82.1 | 372 | 4 | 090HP4 q9unp4 homo sapien |
| 5 | 424.5 | 19.5 | 300 | 4 | 095407 homo sapien |
| 6 | 390.5 | 17.9 | 302 | 13 | 09PUS0 Q9pus0 salvelinus |
| 7 | 314 | 14.4 | 459 | 11 | 063327 mus musculu |
| 8 | 302.5 | 13.9 | 482 | 11 | 088734 mus musculu |
| 9 | 301.5 | 13.8 | 655 | 4 | 073509 homo sapien |
| 10 | 298 | 13.7 | 439 | 4 | 016042 mus musculu |
| 11 | 268.5 | 12.3 | 625 | 11 | 033305 mus musculu |
| 12 | 266.5 | 12.2 | 616 | 4 | 09Y806 q16042 mus musculu |
| 13 | 226 | 10.4 | 355 | 12 | 085308 O9Y806 homo sapien |
| 14 | 224 | 10.3 | 349 | 12 | 057098 O85308 camelpox vir |
| 15 | 222.5 | 10.2 | 349 | 12 | 057305 O57305 camelpox vir |
| 16 | 220 | 10.1 | 349 | 12 | 057284 O57284 camelpox vi |
| 17 | 220 | 10.1 | 349 | 12 | 057097 O57097 camelpox vi |
| 18 | 219 | 10.1 | 349 | 12 | 057110 O57110 variola vir |
| 19 | 218 | 10.0 | 349 | 12 | 057111 O57111 variola vir |

ALIGNMENTS

| RESULT | 1 | ALIGNMENTS |
|--------|--|------------|
| 008712 | PRELIMINARY; PRT; 401 AA. | |
| AC | 008712; 070202; | |
| DT | 01-JUL-1997 (TREMBLrel. 04, Created) | |
| DT | 01-JUL-1997 (TREMBLrel. 04, Last sequence update) | |
| DT | 01-MAY-2000 (TREMBLrel. 13, Last annotation update) | |
| DE | OSTEOCYTE-RELATED PRECURSOR (OSTEOCYTOGENESIS INHIBITORY FACTOR) | |
| DE | (OCIF). | |
| GN | INFRESFIB OR OFG. | |
| OS | Mus musculus (Mouse). | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RP | STRAIN-BALB/C; TISSUE-KIDNEY; | |
| RX | MEDLINE: 97262071. | |
| RA | Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., | |
| RA | Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G., | |
| RA | Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., | |
| RA | Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., | |
| RA | Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., | |
| RA | Sugis S., Boyle W.J. | |
| RT | *osteoprotegerin: a novel secreted protein involved in the regulation | |
| RT | of bone density."; | |
| RT | Cell 89:309-319(1997). | |
| RL | [2] | |
| RN | SEQUENCE FROM N.A. | |
| RP | STRAIN-129/OLA AND NIH SWISS; | |
| RX | MEDLINE: 98382527. | |
| RA | Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T., | |
| RA | Higashio K.; | |
| RT | *Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) | |
| RT | gene and its expression in embryogenesis."; | |
| RL | Gene 215:339-343(1998). | |
| CC | - FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES | |
| CC | OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY | |
| CC | SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO | |
| CC | OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN | |
| CC | OSTEOCLASTS AND OSTEOCLAST PROGENITORS. | |
| CC | - SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM). | |
| CC | - SUBCELLULAR LOCATION: EXTRACELLULAR. | |

| | | | | | | |
|----|-------|------|-----|----|--------|--------------------|
| 20 | 218 | 10.0 | 349 | 12 | 089118 | 089118 variola vir |
| 21 | 217.5 | 10.0 | 349 | 12 | 057099 | 057099 monkeypox v |
| 22 | 216 | 9.9 | 349 | 12 | 089098 | 089098 variola vir |
| 23 | 215.5 | 9.9 | 348 | 12 | 057112 | 057112 variola vir |
| 24 | 215.5 | 9.9 | 348 | 12 | 085407 | 085407 variola vir |
| 25 | 215.5 | 9.9 | 349 | 12 | 057291 | 057291 monkeypox v |
| 26 | 215.5 | 9.9 | 349 | 12 | 057100 | 057100 monkeypox v |
| 27 | 215.5 | 9.9 | 349 | 12 | 057101 | 057101 monkeypox v |
| 28 | 215.5 | 9.9 | 349 | 12 | 057102 | 057102 monkeypox v |
| 29 | 214.5 | 9.8 | 360 | 12 | 057118 | 057118 cowpox viru |
| 30 | 214 | 9.8 | 350 | 12 | 057116 | 057116 cowpox viru |
| 31 | 212.5 | 9.8 | 347 | 12 | 057119 | 057119 cowpox viru |
| 32 | 212 | 9.7 | 348 | 12 | 057277 | 057277 monkeypox v |
| 33 | 212 | 9.7 | 348 | 12 | 057103 | 057103 monkeypox v |
| 34 | 212 | 9.7 | 348 | 12 | 057108 | 057108 monkeypox v |
| 35 | 211.5 | 9.7 | 326 | 12 | 057120 | 057120 cowpox viru |
| 36 | 210.5 | 9.7 | 347 | 12 | 057115 | 057115 cowpox viru |
| 37 | 209.5 | 9.6 | 350 | 12 | 057123 | 057123 cowpox viru |
| 38 | 209 | 9.6 | 349 | 12 | 057109 | 057109 variola vir |
| 39 | 207.5 | 9.5 | 351 | 12 | 057117 | 057117 cowpox viru |
| 40 | 207.5 | 9.5 | 351 | 12 | 073559 | 073559 cowpox viru |
| 41 | 205.5 | 9.4 | 326 | 12 | 057122 | 057122 cowpox viru |
| 42 | 204.5 | 9.4 | 351 | 12 | 057121 | 057121 cowpox viru |
| 43 | 204 | 9.4 | 283 | 4 | 092956 | Q92956 homo sapien |
| 44 | 204 | 9.4 | 283 | 4 | 09TM65 | Q9tm65 homo sapien |
| 45 | 204 | 9.4 | 320 | 12 | 057300 | 057300 ectromelia |

CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
 CC PLACENTA. NOT DETECTED IN SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
 CC 15 TO DAY 17.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: U94331; AAB53708.1; -.
 DR EMBL: AB013898; BAA28269.1; -.
 DR EMBL: AB013903; BAA33388.1; -.
 DR EMBL: AB013899; BAA33388.1; JOINED.
 DR EMBL: AB013900; BAA33388.1; JOINED.
 DR EMBL: AB013901; BAA33388.1; JOINED.
 DR EMBL: AB013902; BAA33388.1; JOINED.
 DR HSSP: P25942; ICDP.
 DR MGD: MGI:109587; OP9.
 DR INTERPRO: IPR000488; -.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF000020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS30017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 201 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 23 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH
 FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH
 FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH
 FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH
 FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
 Query Match 100.0%; Score 2179; DB 11; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2,5e-165;
 Matches: 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 HDNVCSGNREATOKGIDVTLCEBAFFRAVPTKIIIPNMLSVLDSPGTVMNAESVERI 240
 QY 241 KRRSSQEQFOLLKMKHONROEMWKIIIDIDCESSVOHLSNITTDOLAME 300
 DB 241 KRRSSQEQFOLLKMKHONROEMWKIIIDIDCESSVOHLSNITTDOLAME 300
 QY 301 SLPGKTSPIERIEKTRCTSSBOLLKLSLMRLKNGDOQTLGIMALKLHLSHPKT 360
 DB 301 SLPGKTSPIERIEKTRCTSSBOLLKLSLMRLKNGDOQTLGIMALKLHLSHPKT 360
 QY 361 VTHSLRTMRFLHSFTMYRLYOKLFLEMIGNOVOSKISCL 401
 DB 361 VTHSLRTMRFLHSFTMYRLYOKLFLEMIGNOVOSKISCL 401
 RESULT 2
 ID 008727 PRELIMINARY; PRT; 401 AA.
 AC 008727;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF).
 GN TNFRSF1B OR OP9.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE: 97262071.
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hall D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT "osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";
 RL Cell 89:309-319(1997).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC EMBL: U94330; AAB53707.1; -.
 DR HSSP: P25942; ICDP.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF000020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KM Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 201 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.

FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 SQ SEQUENCE 401 AA; 46192 MW; EC6A31F1D4E573A CRC64;

Query Match 95.4%; Score 2079; DB 11; Length 401;
 Best Local Similarity 94.5%; Pred. No. 2.2e-157;
 Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKMLCCALLVLDLIDIEWTOTETLPKYLHYDPETGHOGLCDKCAPGYLKHCHTVRRKT 60
 1 MNKMLCCALLVLDLIDIEWTOTETLPKYLHYDPETGHOGLCDKCAPGYLKHCHTVRRKT 60
 DB 1 MNKMLCCALLVLDLIDIEWTOTETLPKYLHYDPETGHOGLCDKCAPGYLKHCHTVRRKT 60
 QY 61 LCVPCPDHSTYDSWHTSDCVYCSVPCKELOSVKOEKRNTHRVCECEGRYLEIEFCLK 120
 61 LCVPCPDHSTYDSWHTSDCVYCSVPCKELOSVKOEKRNTHRVCECEGRYLEIEFCLK 120
 DB 61 LCVPCPDHSTYDSWHTSDCVYCSVPCKELOSVKOEKRNTHRVCECEGRYLEIEFCLK 120
 QY 121 HRSQPCGSGVAGVAGTPEKNTYCKKCPDGFSGETSSKAPCKHNCSTGLLLQKGNAT 180
 121 HRSQPCGSGVAGVAGTPEKNTYCKKCPDGFSGETSSKAPCKHNCSTGLLLQKGNAT 180
 DB 121 HRSQPCGSGVAGVAGTPEKNTYCKKCPDGFSGETSSKAPCKHNCSTGLLLQKGNAT 180
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIPMLSLVDSLPCTKVNASEVERI 240
 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIPMLSLVDSLPCTKVNASEVERI 240
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIPMLSLVDSLPCTKVNASEVERI 240
 QY 241 KRRHSSQEQTFOLIKLKHONRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
 241 KRRHSSQEQTFOLIKLKHONRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
 DB 241 KRRHSSQEQTFOLIKLKHONRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
 QY 301 SLEPKRTISPEIERTRKCKSSBOLKLSIMRKNGDODLKLMAKLKLSHEPKT 360
 301 SLEPKRTISPEIERTRKCKSSBOLKLSIMRKNGDODLKLMAKLKLSHEPKT 360
 DB 301 SLEPKRTISPEIERTRKCKSSBOLKLSIMRKNGDODLKLMAKLKLSHEPKT 360
 QY 361 VTHSLKRTMRFLSHFTMYRLYQKLFLEMIGNOVOSVKISCL 401
 361 VTHSLKRTMRFLSHFTMYRLYQKLFLEMIGNOVOSVKISCL 401
 DB 361 VTHSLKRTMRFLSHFTMYRLYQKLFLEMIGNOVOSVKISCL 401

RESULT 3
 ID 000300 PRELIMINARY; PRT; 401 AA.
 AC 000300: 060236;

DT 01-JUL-1997 (Tremblere, 04, Last sequence update)
 DT 01-JUL-1997 (Tremblere, 04, Last sequence update)
 DT 01-MAY-2000 (Tremblere, 13, Last annotation update)
 (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
 GN TNFRSF11B OR OPG OR OCIF.

OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;

RA Stimet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luetjens R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Stagg S., Boyle W.J.,
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";
 RT Cell 89:309-319(1997).

RL [2]
 RL SEQUENCE FROM N.A.
 RC TISSUE-LUNG FIBROBLAST;
 RA MEDLINE: 98151033.
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
 RA Tsuda E., Morinaga T., Higashio K.;
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and

RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 RT osteoclastogenesis in vitro.";
 RL Endocrinology 139:1329-1337(1998).

RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 98351569.
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
 RT "Cloning and characterization of the gene encoding human
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Eur. J. Biochem. 254:685-691(1998).

CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEMIX
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
 CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
 CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

DR EMBL: AB008822; BAA32076.1; -;
 DR EMBL: AB008821; BAA32076.1; JOINED.
 DR EMBL: U94332; AAB53709.1; -;
 DR HSSP: P25942; ICDF.
 DR MIM: 602543; -;

DR INTERPRO: IPR001368; -;
 DR PRAM: P700020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KW Glycoprotein; Repeat; Cytokine; Signal.

FT CHAIN 1 21
 FT SIGNAL 1 21
 FT DOMAIN 22 401
 FT REPEAT 23 183
 FT REPEAT 23 63
 FT REPEAT 64 106
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT DOMAIN 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 63 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 98
 FT CARBOHYD 152 152
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT CONFLICT 263 263

SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;
 A -> D (IN REF. 2 AND 3).

Query Match 86.8%; Score 1892; DB 4; Length 401;
 Best Local Similarity 85.6%; Pred. No. 1.5e-142;
 Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;

QY 1 MNKMLCCALLVLDLIDIEWTOTETLPKYLHYDPETGHOGLCDKCAPGYLKHCHTVRRK 59
 1 MNKMLCCALLVLDLIDIEWTOTETLPKYLHYDPETGHOGLCDKCAPGYLKHCHTVRRK 59
 DB 1 MNKMLCCALLVLDLIDIEWTOTETLPKYLHYDPETGHOGLCDKCAPGYLKHCHTVRRK 59
 QY 60 TLVPCPDHSTYDSWHTSDCVYCSVPCKELOSVKOEKRNTHRVCECEGRYLEIEFCL 119
 60 TLVPCPDHSTYDSWHTSDCVYCSVPCKELOSVKOEKRNTHRVCECEGRYLEIEFCL 119
 DB 60 TLVPCPDHSTYDSWHTSDCVYCSVPCKELOSVKOEKRNTHRVCECEGRYLEIEFCL 119
 QY 120 KRRHSSQEQTFOLIKLKHONRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 179
 120 KRRHSSQEQTFOLIKLKHONRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 179
 DB 120 KRRHSSQEQTFOLIKLKHONRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 179

Db 120 KHRSCPPGFGVAGTAPRNTVCKRCPOGFSFNETSSKAPCKKHTNCSVFGILLNOKGNA 179
Qy 180 THDNVCSGNREATQKCGIDVTLCCEAFERFAVPKTIIPNWSLVDSLPGTKNASVER 239
Db 180 THDNCSGSESTQKCGIDVTLCCEAFERFAVPKTIIPNWSLVDSLPGTKNASVER 239
Qy 240 IKRRSSQEQFQOLKIMKHNQNDQEMKIIODIDLCSSVORHSHNLTTEQLALM 299
Db 240 IKRQSSQEQFQOLKIMKHNQNDQEMKIIODIDLCSSVORHSHNLTTEQLALM 299
Qy 300 ESLPKKISPEEIERTRKCKSSQOLKLSLIRKNGDQDYLKGLMAYALKHKTSHPEK 359
Db 300 ESLPKKISPEEIERTRKCKSSQOLKLSLIRKNGDQDYLKGLMAYALKHKTSHPEK 359
Qy 360 TVTSHLRKTRFLSHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
Db 360 TVTOSLKTIRFLSHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401

RESULT 4
Q9HP4 PRELIMINARY; PRT; 372 AA.
Q9HP4:
01-MAY-2000 (TREMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, last sequence update)
01-JUN-2000 (TREMBLrel. 14, last annotation update)
OSTEOPROTEGERIN (FRAGMENT).
Osteoprotegerin (Human).
Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
SEQUENCE FROM N.A.
RC TISSUE-PLACENTA:
He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.,
"Cloning and Expression of Osteoprotegerin from Homo sapiens."
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL; AF134187; AAF20168.1; -
DR INTERPRO; IPR001368; -
DR PFAM; PF000020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT NON-TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 82.1%; Score 1789; DB 4; Length 372;
Best Local Similarity 86.0%; Pred. No. 2.1e-134;
Matches 320; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

22 ELPKRYLHYDEPETHQOLCDKCAPGYLKQCTVRRKTLVPCPDHSTYDSMHTSDECV 81
1 ELPKRYLHYDEPETHQOLCDKCAPGYLKQCTVRRKTLVPCPDHSTYDSMHTSDECV 60
Qy 82 YCSPVCKELQSVKQECNRTNHNVCCEEGRYLEIEFCLKHSRCPGSGVVOAGTPERNTV 141
Db 61 YCSPVCKELQSVKQECNRTNHNVCCEEGRYLEIEFCLKHSRCPGSGVVOAGTPERNTV 120
Qy 142 CKKCDGFFSGSTSKAPRIKTNSTFGLLLIQGNATHDNCVSNRATQKCGIDVT 201
Db 121 CKKCDGFFSGSTSKAPRIKTNSTFGLLLIQGNATHDNCVSNRATQKCGIDVT 180
Qy 202 CEAFERFAVPKTIIPNWSLVDSLPGTKNASVERIKRRSSQEQFQOLKIMKHN 261
Db 181 CEAFERFAVPKTIIPNWSLVDSLPGTKNASVERIKRRSSQEQFQOLKIMKHN 240
Qy 262 RDOEWKRIIDIDLCSSVORHSHNLTTEQLALMSESLPGKISPEEIERTRKCKS 321
Db 241 RDOEWKRIIDIDLCSSVORHSHNLTTEQLALMSESLPGKISPEEIERTRKCKS 300
Qy 322 SEQLLKLSLIRKNGDQDYLKGLMAYALKHKTSHPEKTVTSHLRKTRFLSHSFTMYRLY 381
Db 301 SEQLLKLSLIRKNGDQDYLKGLMAYALKHKTSHPEKTVTSHLRKTRFLSHSFTMYRLY 360

Qy 382 OKLFLEMIGNOV 393
Db 361 OKLFLEMIGNOV 372

RESULT 5
Q95407 PRELIMINARY; PRT; 300 AA.
Q95407:
01-MAY-1999 (TREMBLrel. 10, Created)
01-MAY-1999 (TREMBLrel. 10, last sequence update)
01-MAY-2000 (TREMBLrel. 13, last annotation update)
DECOY RECEPTOR 3.
DCR3 OR TR6.
Osteoprotegerin (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
SEQUENCE FROM N.A.
RX MEDLINE; 99087326.
RA Pictl R.M., Maisters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.I., Gurney A.B., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.,
"Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer."
RL Nature 396:699-703(1998).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE; 99253915.
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Edner R., Kwon B.S.,
"A newly identified member of tumor necrosis factor receptor
superfamily (TR6) suppresses LIGHT-mediated apoptosis."
RL J. Biol. Chem. 274:13733-13736(1999).
DR EMBL; AF104419; AAD03056.1; -
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR000561; -
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KV Receptor
SQ SEQUENCE 300 AA; 32679 MW; F90ADE33718449AF CRC64;

Query Match 19.5%; Score 424.5; DB 4; Length 300;
Best Local Similarity 39.0%; Pred. No. 3.2e-26;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;

26 PLYLHYDEPETHQOLCDKCAPGYLKQCTVRRKTLVPCPDHSTYDSMHTSDECVYCS 85
34 PLYWRDAETGERILVCAQCPGTFVORPCRDSPITCGPCPRHTOPWNLERCNCNV 93
Qy 86 VCKELQSVKQECNRTNHNVCCEEGRYLEIEFCLKHSRCPGSGVVOAGTPERNTVCKK 145
Db 94 LCGEREERARACHATNNAACRGTGFEFHAGFCLEHACCPGAGVIAGTISQNTQCP 153
Qy 146 PDGFFSGSTSKAPRIKTNSTFGLLLIQGNATHDNCVSNRATQKCGIDVTLC 202
Db 154 PDGTTASASSSSQCPHRCNTAGLALNANVGSSSHDILCTSCIGFPLSTVPAEAE--C 211
Qy 203 EAFERFAVPKTIIPNWSLVDSLP 227
Db 212 ERAVIDFAFQDISIKRLQRLQL 236
RESULT 6
Q9PUS0 PRELIMINARY; PRT; 302 AA.
Q9PUS0:
Q9PUS0:

Db 184 STDVCRPHRIS----LAIIPGNASTDAVCA 210

RESULT 9

075509 PRELIMINARY; PRT; 655 AA.
 ID 075509
 AC 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE TNFR-RELATED DEATH RECEPTOR-6.
 DR.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,
 RA Vincenz C., Aggarwal B.B., Dixit V.M.;
 P "Identification and functional characterization of DR6, a novel death
 domain-containing TNF receptor."
 Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF068868; AAC34583.1; -.
 DR INTERPRO: IPR000488; -.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF00020; TNFR_c6; 4.
 DR PFAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 DR SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 13.8%; Score 301.5; DB 4; Length 655;

Best Local Similarity 29.0%; Pred. No. 4.7e-16;
 Matches 91; Conservative 40; Mismatches 150; Indels 33; Gaps 7;

QY 10 LVLDIIMTQOE-----TLPKYLHDPETGHOGLDDCKAPGYLKOCTVRRKTLICV 63
 DB 30 LLLLGELSTTAQBPQKASNLIGTRHVDRAVGVLTDCKPAGYVEHECTSLRCS 89
 QY 64 PCPDHSYDSNHTSDCYVCSPVCKELQSVKQECNRTNHRVCECEGRYLEIEFCLKHRS 123
 DB 90 SCPTGTFTRHNGIEKHCDCQPCWPMEIKLPCALDRECTCPGAFQSNATCAPITV 149
 QY 124 CPSPGGVQACTPERKNTYCKCPDGFSEGTSSKAPCIKHTNCTFGILLIQGNATHDN 183
 DB 150 CPVCGVYKAKGTETEDVRCOCARGTFSVPSVWKCKAYTDCISQNLVVIKPGTKETDN 209
 DB 184 VC-----SGNRATQKCGIDVYLCEAFRFAVPMK-IIPNMLSVYVDSLPGTKVABEVE 238
 DB 210 VCGTLPSSTSTSPGAIAPRPHMETHEVPSSTYVPGKN-----STESSASV 262
 QY 239 RIKRRHSSQEQFOLLKMKHQN-----RDQEMVKKIIDIDLCSSVORHLGHSMLTTEQ 294
 DB 263 RPKVLSSTQETVP-----DNTSSAKGKEDVKTLPNLQVNVHQQGPHRH-----ILK 311
 QY 295 LLAIMESLPGKKIS 308
 DB 312 LIPSEATGGEKSS 325

RESULT 10
 ID 016042 PRELIMINARY; PRT; 439 AA.
 AC 016042;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-JAN-1999 (TREMblrel. 09, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE TNFR-RELATED DEATH RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91370690.
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
 RA Brockschhaus M., Lesslauer W.;
 RT "Two human TNF receptors have similar extracellular, but distinct
 RT intracellular, domain sequences."
 RL Cytokine 2:231-237(1990).
 DR EMBL; S63368; AAB19824.1; -.
 DR HSSP; P25942; ICDF.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF00020; TNFR_c6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 DR SEQUENCE 439 AA; 46090 MW; FEBCB329CC67FF6 CRC64;

Query Match 13.7%; Score 298; DB 4; Length 439;

Best Local Similarity 35.6%; Pred. No. 5.5e-16;
 Matches 62; Conservative 15; Mismatches 75; Indels 22; Gaps 3;

QY 31 YDPETGH-----QLLDCAPGYLKOCTVRRKTLICVPCPDHSYDSNHTSD 78
 DB 10 YAPPGSTCRREYRDDTAQWCCSCSPGOHAKVCTKTSIDTVDCSEDSSTYDLMWVP 69
 QY 79 ECVYCSPVCKELQSVKQECNRTNHRVCECEGRYLE-----EFLCKHSCPGSGVQ 132
 DB 70 ECLSGSRCSDDVETACTEONRITCTCRGWCALSKQBGCLCAPLKRCPGFGVAR 129
 QY 133 AGTERNTVCKKCPDGFSEGTSSKAPCIKHTNCTFGILLIQGNATHDNVCS 186
 DB 130 PGTEISDVYCKPCAPGFTSNSTSTDICRPHQICNVVAI-----PGNSMAYVCT 179

RESULT 11

035305 PRELIMINARY; PRT; 625 AA.

DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
 DE INDUCED CYTOKINE RECEPTOR) (RANK).
 GN TNFRSF1A OR RANK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER EPITHELIUM;
 RX MEDLINE; 98032977.
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function."
 RL Nature 380:175-179(1997).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANK.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; AF019046; AAB86810.1; -.
 DR HSSP; P25942; ICDF.
 DR MGD; MGI:1314891; Tnfrsf1a.
 DR INTERPRO: IPR000561; -.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF00020; TNFR_c6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
 FT SIGNAL 1
 FT CHAIN 31 625 RECEPTOR ACTIVATOR OF NF-KAPPA-B.

FT DOMAIN 31 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 235 POTENTIAL.
 FT DOMAIN 236 625 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 196 4 X TNFR-CYS.
 FT REPEAT 34 70 TNFR-CYS 1.
 FT REPEAT 71 114 TNFR-CYS 2.
 FT REPEAT 115 153 TNFR-CYS 3.
 FT REPEAT 154 196 TNFR-CYS 4.
 FT DISULFID 35 47 BY SIMILARITY.
 FT DISULFID 48 61 BY SIMILARITY.
 FT DISULFID 51 69 BY SIMILARITY.
 FT DISULFID 72 87 BY SIMILARITY.
 FT DISULFID 93 113 BY SIMILARITY.
 FT DISULFID 115 125 BY SIMILARITY.
 FT DISULFID 127 134 BY SIMILARITY.
 FT DISULFID 128 152 BY SIMILARITY.
 FT DISULFID 155 170 BY SIMILARITY.
 FT DISULFID 176 195 BY SIMILARITY.
 FT CARBOHYD 106 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 625 AA; 66621 MW; F8C1872E951D8E CRC64;

Query Match 12.3%; Score 268.5; DB 11; Length 625;
 Best Local Similarity 29.9%; Pred. No. 1.8e-13;
 Matches 88; Conservative 34; Mismatches 123; Indels 49; Gaps 14;

QY 7 CALLVLLDIETWTOETLP--KYLHYPETGQLDCKAPGTYLKQHCVRKTLCPV 64
 19 CVLLVPLQV---TLQVTPCTQERHYE-HLGR--CCSRCEPGVLYSKCTPTSDSVCLP 71
 QY 65 CPHSTYDSMHTSDCYCYCSPVC---KELOSVMQECRTNHRVCECEGRV--LEIEFCL 119
 DB 72 CGPDEYLDSTWNEEDKCL-LHKVCDGAKALVAV-DPGNHTAPRCACAGYHMSDCCCR 129
 QY 120 KHRSCPPGSGVYAGTPERNTVCKCPDFFSGETSSKAPCIKHTNCTGFLLIQKNA 179
 DB 130 RNECAPAGFAQHPLQNLKNTVCTPCLLGFSDFVSTBDCKRPTNCTLGLKLEAHGTT 189
 QY 180 THNVCSGN-----REATQKCGIDVTLCEAFRFAVPTKII----- 216
 DB 190 ESDVYVSSSTLRRPRKQAVYPLSLVLL--LFISVYVAALIFGVYRKGGKALTANL 247
 QY 217 PMLSLVLSLPTKYNASVERIKRRH---SSQEQFOLLKMKHKNROENV 267
 DB 248 WNWVNDACSSLSGNK--ESSGDRACAGSHATSSQOEVCEBILL--MTREKRV 296
 RESULT 12
 ID 09Y606 PRELIMINARY; PRT: 616 AA.
 AC 09Y606;
 DT 01-NOV-1999 (TREMBLER, 12, Created)
 DT 01-NOV-1999 (TREMBLER, 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLER, 13, Last annotation update)
 DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
 INDUCED CYTOKINE RECEPTOR) (RANK).
 GN TNFRSF1A OR RANK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96032977.
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
 RA Tomesko M.E., Rous E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 and dendritic-cell function."
 CC Nature 390:175-179(1997).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN

CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
 CC GLAND.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AF018253; BAB86809.1; -
 DR MIM: 603499; -
 DR INTERPRO: IPR001368; -
 DR PRAM: PR00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS00505; TNFR_NGFR_2; 1.
 KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
 FT SIGNAL 1 22
 FT CHAIN 23 616
 FT DOMAIN 24 212
 FT TRANSMEM 213 233
 FT DOMAIN 234 616
 FT DOMAIN 33 195 4 X TNFR-CYS.
 FT REPEAT 33 69 TNFR-CYS 1.
 FT REPEAT 70 112 TNFR-CYS 2.
 FT REPEAT 113 152 TNFR-CYS 3.
 FT REPEAT 133 195 TNFR-CYS 4.
 FT DISULFID 34 46 BY SIMILARITY.
 FT DISULFID 47 60 BY SIMILARITY.
 FT DISULFID 50 68 BY SIMILARITY.
 FT DISULFID 71 86 BY SIMILARITY.
 FT DISULFID 92 112 BY SIMILARITY.
 FT DISULFID 114 124 BY SIMILARITY.
 FT DISULFID 126 133 BY SIMILARITY.
 FT DISULFID 127 151 BY SIMILARITY.
 FT DISULFID 154 169 BY SIMILARITY.
 FT DISULFID 175 194 BY SIMILARITY.
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 616 AA; 66033 MW; E3DE9A/A08196F81 CRC64;

Query Match 12.2%; Score 266.5; DB 4; Length 616;
 Best Local Similarity 24.4%; Pred. No. 2.6e-13;
 Matches 108; Conservative 54; Mismatches 166; Indels 115; Gaps 21;

QY 5 LCCALLVLLDIETWTOETLP--KYLHYPETGQLDCKAPGTYLKQHCVRKTLCPV 62
 DB 16 LCCALLVLLDIETWTOETLP--KYLHYPETGQLDCKAPGTYLKQHCVRKTLCPV 62
 QY 63 VPCPDISTYDSMHTSDCYCYCSPVC---KELOSVMQECRTNHRVCECEGRV--LEIEF 117
 DB 69 LPCGPDEYLDSTWNEEDKCL-LHKVCDTGAALVAVAG-NSTTPRCACAGYHMSDCCCR 126
 QY 118 CLKHRSCPPGSGVYAGTPERNTVCKCPDFFSGETSSKAPCIKHTNCTGFLLIQKNA 177
 DB 127 CRNTECAPAGFAQHPLQNLKNTVCTPCLLGFSDFVSTBDCKRPTNCTLGLKLEAHGTT 186
 QY 178 NATHNVCSGNREATQK-----CGIDVTLCEAFRFAVPTKII----- 216
 DB 187 TEKSDAVCSSSLPARKPNEPHYLPLGLIIL--LFASVALVAALIFGVYRKGGKALT 243
 QY 217 ---PMLSLVLSLPTKYNASVERIKRRHSS-----QEQTFOLLKMKHKNROENV 257
 DB 244 ANLMWINEACGRLSGDK--ESSGDSVSTHANTFQOQACGCVLLLTLEETFEPMKY 301
 QY 258 KH-----ONRQEWKRIIDIDICESSVOR-----HIGSNLTLEOL 295
 DB 302 PDQGVYCOGTGVGGPYAGGEDARML-SLVSKTEIEDBSFRQMPTEYMDRPSQPTDL 360
 QY 296 LALMESLPGRKISPP--EEIE-----RRRTK-----CNSSEQLKLSLMRIK 335
 DB 361 LFLTE--PSKSPSPSEPLEVGENDSLQCTGTGSSSCNCTEPLCRT----- 411
 QY 336 NGQDPLKGLMALKLTKTSHP 358
 DB 412 --DWTPMSSSENLYQKREVDGHC 432

RESULT 13

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085308
ID 085308 PRELIMINARY; PRT: 355 AA.
AC 085308;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE SECRETED RECEPTOR BINDING TUMOR NECROSIS FACTOR (CRM).
GN CRM.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-BRIGHTON RED;
RC MEDLINE; 83117629.
RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
RT repeated and unique sequence elements."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN-BRIGHTON RED;
RC MEDLINE; 90177240.
RA Parsons B.L., Pickup D.J.;
RT "Transcription of orthopoxvirus telomeres at late times during
RT infection."
RL Virology 175:69-80(1990).
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN-BRIGHTON RED;
RC MEDLINE; 91196263.
RA Hu F.O., Pickup D.J.;
RT "Transcription of the terminal loop region of vaccinia virus DNA 1s
RT initiated from the telomere sequences directing DNA resolution."
RL Virology 181:716-720(1991).
RN [4]
RN SEQUENCE FROM N.A.
RP STRAIN-BRIGHTON RED;
RC MEDLINE; 94378510.
RA Hu F.O., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
RT secreted form of the type II TNF receptor."
RL Virology 204:343-356(1994).
DR EMBL; L08906; AAA60952.1;
DR HSP; P19438; 1TNR.
DR INTERPRO; IPR001368;
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR SEQUENCE 355 AA; 39008 MW; 2C9E5C0D42FA4B3 CRC64;
Query Match 10.4%; Score 226; DB 12; Length 355;
Best Local Similarity 24.1%; Pred. No. 2.2e-10;
Matches 85; Conservative 49; Mismatches 141; Indels 78; Gaps 15;
QY 9 LVLVDDITETGTELPKYLHYDEPG-----HQLLDCKAPGTYLKHQC-IVR 57
DB 6 LLLLSCTIITNSDTP-----HEPSNGKCKDNEYKRRHLLCCSPGTYASRLCDSTKN 60
QY 58 RKTLCVPCPDHSYTDSWMTSDCYVCSFVCKELQSVKQECNRTNHRVCECEGRYLEI-- 115
DB 61 TMTCTPASPSTFTSRNHLPLACLSNCRGDSNOVETRSCTNHRITDCAPGYICFLKG 120
QY 116 ---EFLKHSRCPGSGVQAGTPERTNVCCKCPDGFSETSSKAPCIKHTNCSFGL 171
DB 121 SSGKACVSGQKCGIGYG-VSGHTPTGDVCSPCGLGYSHVSSVDC-EPVPSNTENY 178
QY 172 LLIQKG-NATHDNVC-----SGNRATOKCGIDVTL---CEAFAFRVAVPTKIIPMNL 221
DB 179 IDVELNLPVNDTCTRTTGTGLESISTSELITIMNKKDDPVEFRN-----GYFS 229
QY 222 VLVDLSLP-----TKV---NAESVERIKRRHSQEQFTQLLKKHQRDDEM 266

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DB 230 VLNVAVSGFFTGONRQONISKVCTLNFELKCNKKSYSKQ-----LTKRKNDSDSI 263
QY 267 V-KKIIDIDLCSSVQVRHLGHSNLTE-----QLALMESLPGR 305
DB 284 MPHSESTVLVDCLSSVDIYILXNTWQYEMDTISYHGAVLVDVSHMPGR 336
RESULT 14
ID 057098 PRELIMINARY; PRT: 349 AA.
AC 057098;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRM.
OS Camelox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-SAUDI-M3;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; U87839; AAB94356.1;
DR HSP; P25942; 1CDF.
DR INTERPRO; IPR001368;
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SEQUENCE 349 AA; 37978 MW; 8630BEAED7A584B5 CRC64;
Query Match 10.3%; Score 224; DB 12; Length 349;
Best Local Similarity 24.9%; Pred. No. 3.2e-10;
Matches 76; Conservative 41; Mismatches 126; Indels 62; Gaps 13;
QY 31 YDEPTG-----HQLLDCKAPGTYLKHQCIVRRKKTLCVPCPDHSYTDSWMTSDCY 81
DB 25 YAPANGCKDNEYKRRHMLCCISCPGTYASRLCDSTKNCTCPGSGTFTSRNHLPLAC 84
QY 82 YCSFVCKELQSVKQECNRTNHRVCECEGRYLEI-----EFLKHSRCPGSGVQAGT 135
DB 85 SCNRGDSNOVETRSCTNHRITDCAPGYICFLKGSSGKACVSGQKCGIGYG-VSGHT 143
QY 136 PERFTVCKCPDGFSETSSKAPCIKHTNCSFGLLIQKG-NATHDNVC-----SGNR 169
DB 144 SAGDVICSPGCLGYSTRVGSADKC-EPVPSNTENYIDVELNLPVNDTCTRTTGTGIS 202
QY 190 EATOKCGIDVTL---CEAFAFR--FAVPTKIIPMNLVLDLPGTKVAESVERIKR- 242
DB 203 ESISTSELITIMNKKDDPVEFRYFSVLNV-----ITSGFTTANRQONISKV 252
QY 243 -----RHSSQEQFTQLLKKHQRDDEMVKKIIDIDL---CESSVQVRHLGHS 288
DB 253 CTLNFELKCNKKSYSKQ-----LTKRKNDGIMPS--ETVTLADCLSSVDIYILYS 304
QY 289 NLTE 293
DB 305 NTNTQ 309
RESULT 15
ID 057305 PRELIMINARY; PRT: 349 AA.
AC 057305;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRM.
OS Cowpox virus (CPV).

```


OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MUNICH OPV89/5(CAT), MUNICH OPV 91/1(CAT);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U90233; AAB94389.1; -;
DR EMBL: U90228; AAB94384.1; -;
DR HSSP: P19438; 1TNR.
DR INTERPRO: IPR001368; -;
DR PFAM: PF00020; TNR_C6; 2.
DR PROSITE: PS00652; TNR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS00650; TNR_NGFR_2; 1.
SQ SEQUENCE 349 AA; 38063 MW; 424EE08FDEDD04CF CRC64;

Query Match 10.2%; Score 222.5; DB 12; Length 349;
Best Local Similarity 25.6%; Pred. No. 4, 2e-10;
Matches 81; Conservative 47; Mismatches 144; Indels 45; Gaps 14;
QY 9 LVLVDIIEMTQETLPKYLHPETG-----HQLCDKCAPGYLKQHC--TYR 57
DB 6 LLLLLSCIIILNSDIP-----HEPSNGKCKDNEYRHHLCCLSCPPGYASRLCDSTN 60
QY 58 RKLVCPCPDHSTYDSMHTSDCVYCSPVCKELQSVKQECNRTNHRVCECEGRYLEI-- 115
DB 61 TMTQCTPCSGSGFTSRNNHLPACLSCNGRCDNSQVKTNRSCNTNHRICDCAFGYCLLG 120
QY 116 ---EFCLKHRSCPPSGVVOAGTPERNVYCKKCPDGFSGETSSKAPCIKHTNCSTFGL 171
DB 121 SSGCKACVSGOTKGIYG--VSGHTPTGDDVYCSPCGLGTYSHTVSYDKC--EPVPSNTFNY 178
QY 172 LLIQKG-NATHDVC-----SGNREATQKCGIDVTL---CEAF--FRFVPTKIIIPNW 219
DB 179 IDVEINLYPVNDTSCRTTGTGLSESTSTSELTITMNHKDCDPVFRDGYPSVLNKVATSG 238
QY 220 LSVLVDSLPG--TVNMAEVE--RIKRRHSSQEQTFQLKLMKHQRDQEMV--KKIIDIDL 276
DB 239 FFTGQRRYONISKVCTLNFELKCNKNDSSSKQ-----LTKAKNDALIMPSETVTLVGD 292
QY 277 CESSVQRHLGHSNLTTE 293
DB 293 CLSSVDIYILYSTNTQ 309

Search completed: December 27, 2000, 10:52:38
Job time: 69 sec

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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SM1>
A:Cross-references: GB:M23315; NID:g189185; PIDN:AA59929.1; PID:g189186
R:Kohnu, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring
A:Reference number: A36475; MUID:91045991
A:Accession: A36475
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:X38549; NID:g339757; PIDN:AA63755.1; PID:g339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular
A:Reference number: A48416; MUID:91370690
A:Accession: A48416
A:Status: preliminary
A:Molecule type: mRNA, protein
A:Residues: 23-461 <D2M>
A:Cross-references: GB:S63368; NID:g235648; PIDN:AA19924.1; PID:g235649
R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration
A:Reference number: A36007; MUID:90349572
A:Accession: A36007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A:Cross-references: GB:M5857; NID:g339751; PIDN:AA63362.1; PID:g339752
R:Loetscher, H.; Schlegel, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis
A:Reference number: A23666; MUID:91056048
A:Accession: A23666
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:9010215
A:Accession: B35010
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kunert, P.; Kemper, O.; Wallach, D.
FEBS Lett. 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
A:Reference number: I38094; MUID:95121934
A:Accession: I38094
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CA56324.1; PID:g825701
A:Gene: GDB:TNFR2
A:Status: preliminary
A:Map position: 1p36.2-1p36.2
A:Note: The list of introns is incomplete.
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-32/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: tumor necrosis factor receptor type 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>
F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-279/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>

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F:177,103/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match          14.3%, Score 312, DB 1, Length 461;
Best Local Similarity 34.7%, Pred. No. 2,3e-14;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

QY 8 ALLVLDIIEMTQTQTLPPK--YLHDEPETH-----QLLDRKCAPGYLKH 53
DB 9 ALAAVEEL--WAAAHALPQAAVFTPEAPGPGSTCRREYYQTATMCCSKSPGOHAKVF 66
QY 54 CTVRRKRLICVPCPDHSYTDMSWHTSDECYCSPVCKELOSVMQECNRHTNRYCEEGRYL 113
DB 67 CRTKSDTYDQDSESDSTYQIWMWVPECLISCSGSSDDVEHQACRREGNRLCTCRPGMYC 126
QY 114 EI-----EFLCKHRSCTPGSGVQAGTPERNYVCKKCPDGFSEETISKAPCIHTKCS 167
DB 127 ALSKQEGRLCLPLKRCRPGFGVARGFTETSDVYVCKPCAPGFNTSTSDICRPHQICN 186
QY 168 TEGLLILIOKGNATHDNVCS 186
DB 187 VVAL-----PGNASMDAVCT 201

RESULT 3
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: B38634; A40254; S54816
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A>Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A:Reference number: A38634; MUID:91187885
A:Accession: B38634
A:Molecule type: mRNA
A:Residues: 1-474 <LEW>
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R:Goodwin, R.S.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.;
Mol. Cell. Biol. 11, 3020-3026, 1991
A>Title: Biot. clon. and expression of the type 1 and type 2 murine receptors f
A:Reference number: A40254; MUID:91246168
A:Accession: A40254
A:Molecule type: mRNA
A:Residues: 1-474 <GOO>
A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R:Lisomergis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A:Description: Characterization of the promoter region of the murine p75-TNF receptor
A:Reference number: S54816
A:Accession: S54816
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <KIS>
A:Cross-references: EMBL:X87128; NID:G809043; PIDN:CAA60618.1; PID:G809044
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: cytokine receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <StG>
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F:40-77/Domain: NGF receptor repeat homology <N1>
F:79-120/Domain: NGF receptor repeat homology <NG2>
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match          14.3%, Score 312, DB 2, Length 474;
Best Local Similarity 34.3%, Pred. No. 2,3e-14;
Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;

QY 5 LCCALLVLDIIEMTQETLPKYL-HYDEPETH-----QLLDRKCAPGY 49
DB 6 LMVALVFEQL--WATGHTVPAQVAVLPYKPEPGVGCISQDEYYDRKQMCACAPPGQY 63
QY 50 LKQCHTVRKRLICVPCPDHSYTDMSWHTSDECYCSPVCKELOSVMQECNRHTNRYCEEE 109

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Dd      64 VHFENKTSDFVACACEASMYQWVNNOFRFTCLSCSSCSCTTDVEIRACTKOONFYVCACEA   123
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy     110 GRYLEIEF-----CLNHRSCPSSGYQAOTPERNVYCKCPDGFSGEISSAPCIK   162
       |||:::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     124 GRVCALKTHSHGRCROCMRIKSGPGRGVASSRAPNGNLCKRACAGPTSDTTSIDYCRP   183
       |::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy     163 HTNCSTFGILLIIONGNATHDNVYS    186
       |::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     184 HRICS----ILAIPEGNASDYAVCA    203
       |::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT      4
A#6515
B cell-associated surface molecule CD40, short splice form - mouse
C.Species: Mus musculus (house mouse)
C.Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
Accession: A#6515
Strimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
Immunol. 149, 3921-3926, 1992
A.Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A.Reference number: A#6515; MUID:93094586
A.Accession: A#6515
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: nucleic acid
A.Residues: 1-289 <GR>
A.Cross-references: GB:M63312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N
A.Experimental source: BALB/c, liver
A.Note: sequence extracted from NCBI backbone (NCBP:120357)
C.Comment: For an alternative splice form, see PIR:A46476
C.Superfamily: CD27 antigen; NGF receptor repeat homology
C.Keywords: alternative splicing
F:105-14/Domain: NGF receptor repeat homology <NGF>
```

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Query Match Similarity 12.4% Score 270; DB 2: Length 289;
Match Local Similarity 34.5% Pred. No.1.le-11;
Matches 57; Conservative 26; Mismatches 66; Indels 14; Gaps 5;

QY 27 KYLHDPETGHOLLCDKCAPGYTLKQHCIVRRKTLQVCPDHSYDNTWHTSDC---YVC 83
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 30 QYLH-DGQ-----CCDLLQPGSRILSHCTALEKTKCHPDSEFFSAQNRELRCHQHHNC 83

QY 84 SPVCKELOSVKQECRKHNRHVCECEGRGL--ELIEFLKHSCEPPSGSVQAGTPENNT 140
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      84 EE--NOGLRVKKKEGTAESDTCTCKEGQHCHSKDDEAQAQHPCCIPGQVEMATETD 141

141 VCKKCPDGFSGETSSKAPCIKHTNCTSTFGLLIQGNATHNNVC 185
      || || || || || || || || || || || || || || || || || || || ||
DB 142 VCHPCPVGFSSNQSSLFENCIYPTWSCEDKNLEVLQKGISQTVIC 186

RESULT 5
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C.Species: Mus musculus (house mouse)
C.Date: 18-Jun-1992 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
C.Accession: A46476
R.Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A.Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A.Reference number: A46476; MUID:92105763
A.Accession: A46476
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-305 <TOR>
A.Cross-references: GB:M83312; NID:G1553058
A.Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)
A.Note: this translation is not annotated in GenBank entry M83CD40A, release 113.0
C.Comment: For an alternative splice form, see PIR:A46515
C.Superfamily: CD27 antigen, NGF receptor repeat homology
C.Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

```

[illegible]

```

RESULT      6
A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 17-Mar-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor recept
A:Reference number: S04460; MUID:8935608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:929850; PID:929851
R:Bresch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raj1
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,160/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      12.0%; Score 261; DB 2; Length 277;
Best Local Similarity 33.9%; Pred. No. 4,4e-11;
Matches 58; Conservative 23; Mismatches 74; Indels 16; Gaps 4;

Qy 29 LHYDPETG-----HQLCDKCAPGTYLKHQCTVRKRLCVPCDPHSTYDSMHTSDC 80
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 18 VHPDEPTACRKRQYLINSQCSCSLQPGQKLVSDCTEFETRECLPCGSEFLDTNNRERHC 77
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 81 ---YICSPVCVELSQVQECNRTNHWCECEEGKYL--ELIEFLKHKRSCPGGGVQAG 134
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 HQHKCDPNLG--LRVQOKGTSETDTICTCEGWHCHTSEACSCVLTRHSCSPGFGVQIOA 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 135 TPENKTVKKCPDGFSEFSGETSSKAPCIKHTNCSFFGLLIQNGATHDNVC 185
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 TGVSDTICEPCPVGFEVNSVAPEKCHPWTSCEKFKDVLVQOAGCNKTKDVCV 186
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db      90  LSESPQCDRTDRVNCSTGNYNCLLKGNQRCIGAPQKPCPAGYG-VSGHTRADLTCEK 148
OY      145  CPDGFSEETSKAPCIRHTNCSTFGLLIIOKGNATHDNCSSGNREARQKCIDVTL--- 201
           || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      149  CPPHYTSLSLSPTEKCGTSFNYSIVGFNLKPV-NETSCTTAGHNEVYIKRTEFTVLNMT 207
OY      202  -CEEAF 206
           || : :
Db      208  DCDPVF 213

RESULT      9
GOVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Updon, C.; Maceo, J.L.; Schreiber, M.; McFadden, G.
Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A:Reference number: A40566; MUID:91335768
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <DPR>
A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NG3>
F:106-147/Domain: NGF receptor repeat homology
F:66,181,205,238/binding site: carboxylate (Asn) (covalent) #status predicted

```

| | | | | |
|-----------------------|-----|--|---|-----|
| Db | 76 | RTVATCATCAENSYNHNWNTLTICQLCRP | -CDPVMGLEELIAPCTSRKRTQCRQAPGFCNA | 134 |
| Qy | 113 | --LEIEFLCKHRSCPPGS | -GVVQAGTPERNYTCCKCPDGFSGEGSSKAPCIKHTNCSFF | 169 |
| Db | 135 | WALCTHCELLSDCPEPPGAEIKLDEYVGKGNHCVPCKAGHFONTSSP | SPARCOPTHRCENO | 194 |
| Qy | 170 | GLLLLOKGNATHDNYCSGNRE | 190 | |
| Db | 195 | GLVEAPGTAOSTTCKNPLE | 215 | |
| RESULT | 8 | | | |
| B43692 | | T2 protein - rabbit fibroma virus | | |
| C:Species: | | rabbit fibroma virus, Shope fibroma virus | | |
| C:Date: | | 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 | | |
| C:Accession: | | B43692 | | |
| Clon., C.: | | Delange, A.M.; McFadden, G. | | |
| ology | | 160, 20-30, 1987 | | |
| A:Title: | | Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric | | |
| A:Reference number: | | A43692; MUID:87321103 | | |
| A:Accession: | | B43692 | | |
| A:Status: | | preliminary | | |
| A:Molecule type: | | DNA | | |
| A:Residues: | | 1-325 <UPR> | | |
| A:Cross-references: | | GB:M17433 | | |
| C:Subfamily: | | myxoma virus T2 protein; NGF receptor repeat homology | | |
| F:64:105/Domain: | | NGF receptor repeat homology <NK2> | | |
| F:106-147/Domain: | | NGF receptor repeat homology <NG3> | | |
| Query Match | | 10.7%: Score 233.5; DB 2: Length 325; | | |
| Best Local Similarity | | 31.7%: Pred. No. 4.2e-09; | | |
| Matches | 59; | Conservative 19; Mismatches 91; Indels 17; Gaps 5; | | |
| Qy | 36 | GHQ-----LLCDKCAPGTYLKQHCYRRKTLCPCPDHSYDTSWMTSDECVYCSPYKCEL | 90 | |
| Db | 30 | GHDYKDGICACASCHPGFYASRLCGSGSWTVCSPCEDGTFSTAHNAPACVSCRGPCIGH | 89 | |
| Qy | 91 | QSVKRECNATHNRVCECEGRILEIF-----FCLKHRCSPGSGVYVAGTPEARNVCKK | 144 | |

A:Reference number: 546868
A:Accession: 546888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics:
Gene: G4R
Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:62-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 10.0% Score 217; DB 2; Length 349;
Best Local Similarity 23.2% Pred. No. 6.2e-08;
Matches 92; Conservative 51; Mismatches 169; Indels 84; Gaps 17;

OY 4 WLCCALLVLDLIDIEWTQETLPPKYLHYDPE-TGHQLLDCKCAPGTYLKOHCTVRRKTLG 62
DB 11 FLSCIIINGRDAAPYT-----PPNGCKKDTYKRRNNLCLCSPGTYSRLDCKSTNTQC 65
63 VPCPHSTDSMHTSDDECYVCSFVCKELQSAKQECNFRTHNRVCBCEBGRILEI-----E 116
66 TPCGSGFTSRNNHLPACISCNCRNSNOVETRSNTTHNRICECSPGYCLKSSGCK 125
OY 117 FCLKRSQPPSGGVQAGPERNTVCKCKPOGFEFGEISSKAPCKIKHNSFFGLLLO- 175
DB 126 ACVSQTKCGIGTG-VSGHTSVGDVICSFGGFTYSHTVSSADCKEPPVP-NTEFNIDVEI 183
OY 176 KGNATHDVCSGNREATORCKGIDVTLCBEAFRFRAVPTKILPNMLSVLDSLPGRVNAE 235
DB 184 TLTPYNDVDSCT-----RTTTTGLSE-----SILTSEL----- 210
OY 236 SVERIKRRHS-----QDTFQLK-----LWKHONDQENVKIITODIDLCSSVGRH 284
211 ---TTMHTDPCNPVFEREFSVLNKVAISGFFTGENTRYONISK-----VCTLNFELK 260
OY 285 LGSNLTTEQALLALMESLPGKRIPELEIERTKTKTKSSSQQLKLKLSLWRIRKGDODTLKG 344
DB 261 CNNGKSSFKOLAKAND--DGMMSSEVTYTLAGDLSVDIYLXSNNAODYETDLS- 317
OY 345 LMYALKHL--KTSHP-----KVTWHSLRKTMREL 372
DB 318 --YRYGNVLDDDSHMPGSCNTHKPIITNS--KPTREL 349

RESULT 11
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: D72175
R:Shchelkunov, S.N.; Totemuhin, A.V.; Gutorov, V.V.; Safonov, P.F.; Masung, R.F.; Lopatin, R.; Shchelkunov, S.N.; Blinov, V.M.; Sandakhchev, L.S.
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: D72175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759
A:Experimental source: strain Garcia-1966

C:Genetics: G2R
C:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 9.9%; Score 216; DB ?; Length 349;
Best Local Similarity 23.2%; Pred. No. 7.3e-08;
Matches 92; Conservative 51; Mismatches 169; Indels 84; Gaps 17;

4 WLCCALLVLDLIDIEWTOETLPPRYLHYDE-IGHOLLCDKCAAGTYLKQCHTVRRKTLG 62
11 FLSCIIRGRDAAPYT-----PPNGCKKDTEYKRHNLCCLSCPPGTAYASRLCDSTKTYQC 65
63 VPCPHSTDSMHSDECVYCSFYCKELQSYKQECNFRHNHNVCCCEGRILEI-----E 116
66 TPCGSGITTSRNNHLPALCLSCNGRCNSNOVTRSCNTHNHCISCPGYLLGLGSSGCK 125
117 FCLKHSRCPSPSGVQAGTAPRNTVCKKCPGFGSGETSSKAPCIKHTNCSFTGLLIQ- 175
126 ACVSOTKCGIGYG-VSGHTSVGDVYCSPCGGTSTSYVSSDKCEPVPN-NTFWYIDVEI 183
176 KGNATHDVCNCGNREPAQCKGIDVTLCEAEFRFAVPTKIIIPNLSVLDSPGTXYNAE 235
184 TLYPNDISCT-----RTTTGLSE-----SILTSEL----- 210
236 SVERKKRHS-----QQTQFLK-----LMKHQNDQEMVKKIIDDIDLCSSVORH 284
211 ---TTNNHTCNPYFREYPSVLNKVATSGFTGGENRYONISK-----VCTLNEIK 260
285 LGHSNLTQELLALMESLPKGIISPEIERTKCKSSEQLKLSLRIRKNGODPLKG 344
261 CNNGKSSFKQLTKAKND--DGMHSEYVTLAGCLSSVDYIILXSNMADYETDTIS- 317
345 LMYALKHL-KTSHP-----KVTNHSRKTMFPL 372
318 --YRVGNVLDSDSHMPCSDIHKLITNS--KPTREPL 349

RESULT 12
228623
hypothetical protein G2R - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: J28623
R:Masung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Uterback, T.R.; Knight, J.C.; Au
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: 220488; MUID:94088747
A:Accession: J28623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-reference: EMBL:L22579; PIDN:AAA0933.1
A:Experimental source: strain Bangladesh 1975
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 9.9%; Score 215.5; DB 2; Length 348;
Best Local Similarity 23.1%; Pred. No. 7.9e-08;
Matches 87; Conservative 47; Mismatches 156; Indels 87; Gaps 16;

31 YDPETG-----HQLCDKAPGTYLKQCHTVRRKTLGCPDPHSYTDSSWHTSDECV 81
24 YTPNGKCKDTEYKRHNLCCLSCPPGTAYASRLCDSTKTYQCCTPCGSGTFTSRNNHLPACL 83
82 YCSFYCKELQSYKQECNFRHNHNVCCCEGRILEI-----EFLKHSRCPSPSGVQAGT 135
84 SCNGRCNSNOVTRSCNTHNHCISCPGYLLGLGSSGCAACVSYQTKGIGYG-VSGHT 142
136 PERNVYCKKCPDGFSGETSSKAPCIKHTNCSFTGLLIQ-KGNATHDVCNCGNREPAQCK 194
143 SVGDVYCSPCGGTSTSYVSSDKCEPVPN-NTFWYIDVEITLYPVDISTCT-----RTTT 197

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OY 195 CGIDVLTCEFAFFFAVPTKRIIPMWLSVLDLPSTGVNNAESVERIKRRHS-----OEQ 249
D 198 TGLSE-----SILISEL-----TITMNRDPCNPFREE 225
OY 250 TFOLEK-----LWKHONRODEWVKKIIQDIDLCSSVORHAGHSNLTTEOLLALMESLP 303
D 226 YFSLNKNVANSGETGNGRKNISK-----VCTLNEIKNKNGSGSFOLTAKN-- 276
OY 304 GKKSPEIEFTKTKCKSSSEOLLKLSLWRIKNGDQDLKLTAKHL--KTSHP-- 358
D 277 DGMMSHEVTLACDCLSSVDIYLYSNTNADYETDPIIS---YRVGNVLDLDDSHMPSGC 333
OY 359 ---KTVTHSLKTKMRFL 372
D 334 NIKPITNS--KPTREFL 348

RESULT 13
GOHUN
Nerve growth factor receptor precursor, low affinity - human
N:Alternate names: NGF receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999
C:Accession: A25218; A60204; S21689; I57638
R:Johnson, D.; Iannan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A:Title: Expression and structure of the human NGF receptor.
A:Reference number: A25218; MUID:87051725
A:Accession: A25218
A:Molecule type: mRNA
A:Residues: 1-427 <JOH>
A:Cross-references: GB:M14764; NID:g189204; PIDN:AA59544.1; PID:g189205
R:Mariano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A:Reference number: A60204; MUID:87085574
A:Accession: A60204
A:Molecule type: protein
A:Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A:Experimental source: melanoma cell line A875
A:Note: This sequence has been corrected by a note added in proof to follow the nucleotide
R:Yissavajjhala, P.; Leszyk, J.D.; Lin-Goetze, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor
A:Reference number: S21689; MUID:92198017
A:Accession: S21689
A:Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>
R:Sehgal, A.; Patil, N.; Chao, M.
Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor
A:Reference number: I57638; MUID:89096903
A:Accession: I57638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:g189206; PIDN:AA36363.1; PID:g189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates
C:Comment: This receptor undergoes both N- and O-linked glycosylation.
C:Genetics:
A:Gene: GDB:NGFR
A:Cross-references: GDB:120234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology;
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
F:29-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>

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F:109-147/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Region: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 199; DB 1; Length 427;
Best Local Similarity 31.7%; Pred. No. 1,4e-06;
Matches 52; Conservative 25; Mismatches 71; Indels 16; Gaps 6;

OY 9 LTVLIDIIEMTQETLPKYLHYDPETGHQLDCKAPGYTLKOHCHVRKRLCVPDPH 68
D 17 LLLLVSLGAKKACPTGLYTHSGE-----CKACMLGEGVAKQPCGA-NQYCEPCIDS 70
OY 69 -SYDSWHTSDEVCYCSPVCKELQSVKQECNRRTHNRVCEDEGRYLE-----IEFCLKHR 122
D 71 VTFSDVVSATEPKPCPE-CVGLQSMGAPCEVADDAVCRCAYGVODETGRCEAC---R 126
OY 123 SCPPGSGVQAQGPRTNVTCKKCPDFGSEFTSKAPCIRHTNC 166
D 127 VCEAGSGLVFSCDQKNTVCECPDGYSDANHVDPCLPCTVC 170

RESULT 14
A26431
Nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Raddeke, M.T.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R:Metzls, M.; Timmusk, T.; Allikmets, R.; Saarna, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retin
A:Reference number: PH1229; MUID:93077038
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C:Comment: The cysteine-rich region of the extracellular domain may form part or all
C:Comment: This protein is thought to form a high-affinity receptor when it associate
C:Genetics:
A:Insertions: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology;
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <MAT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Region: serine/threonine-rich
F:252-273/Domain: transmembrane #status predicted <MEM>
F:274-425/Domain: intracellular #status predicted <INT>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 197.5; DB 1; Length 425;
Best Local Similarity 22.1%; Pred. No. 1,7e-06;
Matches 95; Conservative 59; Mismatches 152; Indels 123; Gaps 19;

OY 9 LTVLIDIIEMTQETLPKYLHYDPETGHQLDCKAPGYTLKOHCHVRKRLCVPDPH 68

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Db 18 LLLILGSSGAKKCTCTGLYTHSGE-----CCACNNGEAVAPCGA-NQTVCEPCIDN 71
QY 69 -SYTDSMHTSDECVYCSPVCKELOSVAQECNRTHNRVCECEBGRYLEIE--FCLKHRSKP 125
Db 72 VTFSDVVSATPCPKPTE-CIGLOSMAPCAVEADAVRCARAYGQDEBTEHCACSVCE 130
QY 126 PGSGVQAGTPERTNVCKKCGDFFSGTSSKAPCIRKNTSGFLLILOGNATHDNYC 185
Db 131 VGSGLVSCODKONTVCECEGEGTSDANVHVPCLPCTVEDTERQL----- 178
QY 186 SGNEATOKGIDVTLCCEAFERF-----AVPRK--IIPNMLSVL 223
Db 179 ---RECTPMADAE---CEIIGRMIPRSTPPGSDSTAPSGEBVPEPQDLVSTVADM 232
QY 224 VDSLPGTKVNAESVERIKRRHSQE-----QTFOLKLWK--HONRDOE 265
Db 233 VTTVMG-----SSQPVYTRGTDNLIIPYCSILAAVVYGLVAYIAFRMNSCKONKOGA 286
QY 266 MVKKIIQ-----DIDCESSVQRHLGHSNLTTFQLLA---LMESLPGRK-- 306
Db 287 NSRPVNOTPPEGEKLSDSGISVDSQSLMDQHTOTPASGQALKGDGNTLXSLPTKRE 346
QY 307 -----ISPEIER-TRKTKCKSSEQLKLSLRIRKNGDOD--TLKG 344
Db 347 EVERKLNQDTRHRLAGELGYPERHIDSTHEAC---PYRALLASW---GQDSATIDA 398
QY 345 LMYALKHLK 353
Db 399 LLAALRRIQ 407

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RESULT 15

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JN0006
nerv growth factor receptor, low affinity precursor - chicken
N:Alternate names: NGF receptor
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0006; A60504
R:Large, T.H.; Meskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid
Neuron 2, 1123-1134, 1989
A:Title: Structure and developmental expression of the nerve growth factor receptor in t
A:Reference number: JN0006; MUID:90165579
A:Accession: JN0006
A:Molecule type: mRNA
R:Residues: 1-416 <LAR>
Experimental source: embryonic chick brain
Heuer, J.G.; Patemie-Nahie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A:Title: Structure and developmental expression of the chicken NGF receptor.
A:Reference number: A60504; MUID:90152140
A:Accession: A60504
A:Molecule type: mRNA
A:Status: preliminary; not compared with conceptual translation
A:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Superfamily: This protein is thought to form a high-affinity receptor when it associates w
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-416/Domain: nerve growth factor receptor #status predicted <MAT>
F:21-239/Domain: extracellular #status predicted <EXT>
F:24-57/Domain: NGF receptor repeat homology <NG1>
F:59-100/Domain: NGF receptor repeat homology <NG2>
F:101-139/Domain: NGF receptor repeat homology <NG3>
F:141-181/Domain: NGF receptor repeat homology <NG4>
F:189-237/Region: serine/threonine-rich
F:240-261/Domain: transmembrane #status predicted <MEM>
F:262-416/Domain: intracellular #status predicted <INT>
F:52/Binding site: carbohydrate (asn) (covalent) #status predicted

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Query Match      8.4%; Score 184; DB 1; Length 416;
Best Local Similarity 30.9%; Pred. No. 1.4e-05;
Matches 46; Conservative 28; Mismatches 67; Indels 8; Gaps 6;
QY 41 CDKCAPGTLYKQKCTVRRKTLVCPDPH-SYTDSMHTSDECVYCSPVCKELOSVAQECNR 99
Db 36 CKACNLGEGVYQPCGV-NQTVCEPCIDSVTYSATPECPKCTO-CVGLHSMAPCQE 93
QY 100 THNRVCECEBGRYLEIE---CLKHRSKPGSGVQAGTPERTNVCKKCGDFFSGTSS 156
Db 94 SDAVVCRCAYG-YFQDELSGSCKECSICEVGFGLMFPQRSDTVCEBCEGTFESDANF 152
QY 157 KAPCIKHTNCTFGLLILOGNATHDNYC 185
Db 153 VDPCLPCTICEE-NEVMKECTATSDAEC 180

```

Search completed: December 27, 2000, 10:54:37
 Job time: 188 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:51:38 ; Search time 24.16 Seconds
(without alignments)
530.262 Million cell updates/sec

Title: US-09-389-545-2

Sequence: 1 MNKWLCCALLVLDIIEWT.....OKFLEMIGNOVSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 314 | 14.4 | 461 | 1 | TNR2_HUMAN |
| 2 | 312 | 14.4 | 474 | 1 | TNR2_MOUSE |
| 3 | 270 | 12.4 | 289 | 1 | CD40_MOUSE |
| 4 | 261 | 12.0 | 277 | 1 | CD40_HUMAN |
| 5 | 244 | 11.2 | 435 | 1 | TNRC_HUMAN |
| 6 | 233.5 | 10.7 | 335 | 1 | VT2_SFVRA |
| 7 | 228 | 10.5 | 269 | 1 | CD40_BOVIN |
| 8 | 220 | 10.1 | 349 | 1 | VT2_MXYVL |
| 9 | 217 | 10.0 | 349 | 1 | VC22_VAPV |
| 10 | 206 | 9.5 | 415 | 1 | TNRC_MOUSE |
| 11 | 199 | 9.1 | 427 | 1 | NGFR_HUMAN |
| 12 | 197.5 | 9.1 | 425 | 1 | NGFR_RAT |
| 13 | 190.5 | 8.7 | 333 | 1 | FASA_BOVIN |
| 14 | 184 | 8.4 | 416 | 1 | NGFR_CHICK |
| 15 | 182 | 8.4 | 335 | 1 | FASA_HUMAN |
| 16 | 177 | 8.1 | 256 | 1 | 41BB_MOUSE |
| 17 | 176 | 8.1 | 332 | 1 | FASA_PIG |
| 18 | 167 | 7.7 | 461 | 1 | 41BB_HUMAN |
| 19 | 165.5 | 7.6 | 255 | 1 | TNR1_PIG |
| 20 | 163 | 7.5 | 271 | 1 | OX40_RAT |
| 21 | 161.5 | 7.4 | 454 | 1 | OX40_MOUSE |
| 22 | 160 | 7.3 | 455 | 1 | TNR1_HUMAN |
| 23 | 160 | 7.3 | 471 | 1 | TNR1_BOVIN |
| 24 | 153 | 7.0 | 461 | 1 | TNR1_RAT |
| 25 | 152.5 | 7.0 | 272 | 1 | OX40_MOUSE |
| 26 | 151 | 6.9 | 277 | 1 | OX40_HUMAN |
| 27 | 147.5 | 6.8 | 324 | 1 | FASA_RAT |
| 28 | 143 | 6.6 | 327 | 1 | FASA_MOUSE |
| 29 | 139 | 6.4 | 395 | 1 | CD30_HUMAN |
| 30 | 133 | 6.1 | 1786 | 1 | LMB1_HUMAN |
| 31 | 130.5 | 6.0 | 1789 | 1 | LMB1_MOUSE |
| 32 | 126.5 | 5.8 | 260 | 1 | CD27_HUMAN |
| 33 | 125 | 5.7 | 1680 | 1 | FUR2_DROME |

| | | | | | | |
|----|-------|-----|------|---|------------|--------------------|
| 34 | 120.5 | 5.5 | 250 | 1 | CD27_MOUSE | P41272 mus musculu |
| 35 | 120.5 | 5.5 | 291 | 1 | FBN2_HUMAN | P35556 homo sapien |
| 36 | 119.5 | 5.5 | 1639 | 1 | LMG1_DROME | P15215 drosophila |
| 37 | 119 | 5.5 | 1609 | 1 | LMG1_HUMAN | P11047 homo sapien |
| 38 | 118 | 5.4 | 3712 | 1 | LMA_DROME | 000174 drosophila |
| 39 | 116.5 | 5.3 | 915 | 1 | PAC6_MOUSE | 004592 mus musculu |
| 40 | 116 | 5.3 | 1955 | 1 | AGRI_CHICK | P31696 gallus gall |
| 41 | 116 | 5.3 | 3084 | 1 | LMAI_MOUSE | P19137 mus musculu |
| 42 | 116 | 5.3 | 3106 | 1 | LMAI_MOUSE | Q60675 mus musculu |
| 43 | 115.5 | 5.3 | 713 | 1 | TS4_GIALA | P21849 giardia lam |
| 44 | 115.5 | 5.3 | 1607 | 1 | LMG1_MOUSE | P02468 mus musculu |
| 45 | 115 | 5.3 | 417 | 1 | MSL1_HUMAN | Q93038 h wal-1 pro |

ALIGNMENTS

| RESULT | ID | SEQUENCE | STANDARD | PRT | AA |
|--------|---|----------|----------|-----|----|
| 1 | TNR2_HUMAN | | | | |
| 1 | TNR2_HUMAN | | | | |
| AC | P20333 | | | | |
| DT | 01-FEB-1991 (Rel. 17, Created) | | | | |
| DT | 01-AUG-1991 (Rel. 40, Last annotation update) | | | | |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) | | | | |
| DE | TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TNFRI) (P80) (TNF-R2) (CD120B) (ETANERCEPT) | | | | |
| DE | TNFRSF1B OR TNFR2 OR TNFR. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE: 90260639. | | | | |
| RA | Kohn T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., | | | | |
| RA | Hale K.K., Squares C.H., Thompson R.C., Vannice J.L.; | | | | |
| RT | "A second tumor necrosis factor receptor gene product can shed a | | | | |
| RT | naturally occurring tumor necrosis factor inhibitor."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE: 96299745. | | | | |
| RA | Beitinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., | | | | |
| RA | Leopastier D., Stallard B.J., Goeddel D.V., Desauvage F.J.; | | | | |
| RT | "Physical mapping and genomic structure of the human TNFR2 gene."; | | | | |
| RL | Genomics 35:94-100(1996). | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE. | | | | |
| RX | MEDLINE: 90349572. | | | | |
| RA | Heiler R.A., Song K., Onasch M.A., Fischer W.H., Chang D.; | | | | |
| RA | Ringold G.M.; | | | | |
| RT | "Complementary DNA cloning of a receptor for tumor necrosis factor | | | | |
| RT | and demonstration of a shed form of the receptor."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990). | | | | |
| RN | [5] | | | | |
| RP | SEQUENCE OF 27-31. | | | | |
| RX | MEDLINE: 90110215. | | | | |
| RA | Engelmann H., Novick D., Wallach D.; | | | | |
| RT | "Two tumor necrosis factor-binding proteins purified from human | | | | |
| RT | urine. Evidence for immunological cross-reactivity with cell surface | | | | |
| RT | tumor necrosis factor receptors."; | | | | |
| RL | J. Biol. Chem. 265:1531-1536(1990). | | | | |
| RN | [6] | | | | |
| RP | SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362. | | | | |
| RX | MEDLINE: 91056048. | | | | |

RA Loetscher H., Schlaeger E.J., Lahn H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.,
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RP [7]
 RP CHARACTERIZATION.
 RX MEDLINE: 9301600A.
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.,
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TNF2 COMPLEX.
 RX MEDLINE: 99221490.
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.,
 RT "Structural basis for self-association and receptor recognition of
 RT human TNF2.";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
 CC WEITH-AYENST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
 CC PORTION OF TNF2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
 CC -1- SIMILARITY: CONTAINS A LA-NGRP/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME-PROV. NOTE-CD guide CD120b entry;
 CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROV/CD/CD120B.HTM"
 CC -1- DATABASE: NAME-Enbrel; NOTE-Clinical information on Enbrel;
 CC WWW="HTTP://WWW.ENBRELINFO.COM/".
 CC -----
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 CC -----
 DR EMBL: M32315; AAA59929.1; -;
 DR EMBL: M3857; AAA63262.1; -;
 DR EMBL: U52156; AAC50622.1; JOINED.
 DR EMBL: U52157; AAC50622.1; JOINED.
 DR EMBL: U52158; AAC50622.1; JOINED.
 DR EMBL: U52159; AAC50622.1; JOINED.
 DR EMBL: U52160; AAC50622.1; JOINED.
 DR EMBL: U52161; AAC50622.1; JOINED.
 DR EMBL: U52162; AAC50622.1; JOINED.
 DR EMBL: U52163; AAC50622.1; JOINED.
 DR EMBL: U52164; AAC50622.1; JOINED.
 DR EMBL: M55994; AAA36755.1; -;
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR PDB: 1CA9; 12-APR-99.
 DR MIM: 191191; -;
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00500; TNFR_NGFR_2; 4.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Phosphorylation; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.

FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 258 287 POTENTIAL.
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 201 4 X TNFR-CYS.
 FT REPEAT 39 76 TNFR-CYS 1.
 FT REPEAT 77 118 TNFR-CYS 2.
 FT REPEAT 119 162 TNFR-CYS 3.
 FT REPEAT 163 201 TNFR-CYS 4.
 FT DISULFID 40 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 110 BY SIMILARITY.
 FT DISULFID 100 118 BY SIMILARITY.
 FT DISULFID 120 126 BY SIMILARITY.
 FT DISULFID 134 143 BY SIMILARITY.
 FT DISULFID 137 161 BY SIMILARITY.
 FT DISULFID 164 179 BY SIMILARITY.
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 141 141 R -> P (IN REF. 4).
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
 FT CONFLICT 196 196 A -> T (IN REF. 4).
 FT SEQUENCE 461 AA; 48316 MM; 603B580ECD67636F CRC64;
 SQ
 Query Match 14.48; Score 314; DB 1; Length 461;
 Best Local Similarity 34.78; Pred. No. 1,9e-15;
 Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;
 OY 8 ALVYLDIIEWTQETLPPK--YLHYDEPETH-----QLCDKCAPGTLYKOH 53
 DB 9 ALAVGLEL--WAHAHALPAQVATFTPAPEPSTCRLEKYDQTQNMCKSCSPQGHAKVF 66
 OY 54 CTVRKRLVCPPHSYTDSWHTSDECVYCSPVCKELQSVKQECNFRTHRVCEBEGRYL 113
 DB 67 CKTSDFVDCSDCEDSTYQLWNNWPECLSCGRSSQVETQACTREONRICTCRPGWYC 126
 OY 114 EI-----EPLKTRHSCPPSGGVQAGTPERNYCKKCPDGFSEGSRAKPCIKHTNCS 167
 DB 127 ALSKQEGRLCLAPLKCKPGFGVAPGTETSDVYCKPCAPGTFSNTTSTIDICRPHQICN 186
 OY 168 TFGLLILQGNATHDNYCS 186
 DB 187 VVAI-----PGNASRDVCT 201
 RESULT 2
 ID TNFR2_MOUSE STANDARD; PRT; 474 AA.
 AC P25119; P97893;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
 GN TNFRSF1B OR TNFR2 OR TNFR-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 91187885.
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.,
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 91246168.
 RX Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.,


```

FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 289 AA; 32111 MM; C791CB6D2FEA574E CRC64;

Query Match 12.4%, Score 270; DB 1; Length 289;
Best Local Similarity 34.5%, Pred. No. 1,5e-12;
Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

OY 27 KYLHDPPEGHQLDCKAPGTYLKHOCIVRRKTCVPCPDHSYDMSHTSDEC---YYC 83
DB 30 QYLH-DGQ-----CCDLQOPGSRLLSHKTALEKTCQHPDSESEFAQNNRETRCQHNRIC 83
OY 84 SPVCKELOSVKOECNRTHNRVCEEGRYL---ETIEFLKHRSCPPGSGVQAGTPERT 140
DB 84 EP--NQGRLRVKKEGTAESDVTCTCKEGGCHTSKDEACAGQHPCIPGVGMATETTDT 141
OY 141 VCKKPPDGFSGEETSSKAPCIHTNCSITFGLLIORKNATHDNC 185
DB 142 VCHPCPVGFSSNSSLFEKCYPMWCEDECKNLELQKTSQTNVIC 186

RESULT 4
CD40_HUMAN STANDARD: PRT: 277 AA.
ID CD40_HUMAN
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
DE TNFRSF5 OR CD40.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 89356608.
RX Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:11403-11410(1989).
RN [2]
RN 3D-STRUCTURE MODELING OF 24-144.
RP MEDLINE: 97189482.
RX Bajorath J., Amuffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [3]
RN 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RP MEDLINE: 98266353.
RX Singh U., Gaidar E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RX Zhang Z., Nasmith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGRF/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD40.HTM".
CC -----
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DR   EMBL, X60592; CAA43045.1; -.
DR   PIR, S04460; S04460.
DR   PDB, 1CDF; 01-APR-97.
DR   MIM, 109535; -.
DR   INTERPRO: IPR001368; -.
DR   Pfam: PF000020; TNFR_C6; 4.
DR   PROSITE: PS00652; TNFR_NGFR_1; 1.
DR   PROSITE: PS50050; TNFR_NGFR_2; 4.
KW   Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW   3D-structure.
FT   SIGNAL          1      19      POTENTIAL.
FT   CHAIN           20     277     CD40L RECEPTOR.
FT   DOMAIN          20     193     EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM       194     215     POTENTIAL.
FT   DOMAIN          216     277     CYTOPLASMIC (POTENTIAL).
FT   DOMAIN          225     187     4 X TNFR-CYS.
FT   REPEAT          25      60      TNFR-CYS 1.
FT   REPEAT          61     103      TNFR-CYS 2.
FT   REPEAT          104     144      TNFR-CYS 3.
FT   REPEAT          145     187      TNFR-CYS 4.
FT   REPEAT          145     187
FT   DISULFID        26      37
FT   DISULFID        38     51
FT   DISULFID        42     59
FT   DISULFID        61     77
FT   DISULFID        83     103
FT   DISULFID        105     119
FT   DISULFID        111     116
FT   DISULFID        125     143
FT   CARBOHYD        153     153
FT   CARBOHYD        180     180
FT   SEQUENCE        277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;
SQ
Query Match          12.0%; Score 261; DB 1; Length 277;
Best Local Similarity 33.9%; Pred. No. 6,4e-12;
Matches 58; Conservative 23; Mismatches 74; Indels 16; Gaps
4;
OY   29 LHYDETG-----HQLLDKCAPGYLYLQHCTVRRKTLCPDPDSYDTSWHTSDEC 80
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   18 VHPPEPTACREKQYLINSQCCSLCPGQKIVSDCTEFETETECLEPGESFELDTWNRTHC 77
OY   81 ---VYCSVCKELQSVKRDCKNTHRVQCECEGRLL---EIFPCLAKHSCEPGSGVYQAG 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   78 HQHKACDNLG--LRVQKGKTSSETPTITCEGWMGHTSEACSVLHRSCSPGFVKQIA 135
OY   135 TPRTVYCKCPDGFSEGTSSKAPCIKHTKNSFTGILLIQGNATHDNYC 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   136 TGVSDTICEPCVGFSSVNSAFECHEWTSCEITDLYVQAGTKTIDVYC 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      5
TNRG_HUMAN  STANDARD:      PRT:      435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   LYMPHOXOIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE   2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN   LTR OR TNFR OR TNFRSF3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE: 93252381.
RA   Baens M., Chaffaret M., Cassiman J.J., den Bergh H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).

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RN [2]
 RP FUNCTION.
 RA MEDLINE: 94225209.
 RX Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
 RA Ehrenfeld B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 RT "A lymphotoxin-beta-specific receptor."
 RL Science 264:707-710(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC
 CC EMBL: L04270; AAA36757.1; -
 CC DR HSSP: P25942; 1CDF.
 CC DR MIM: 600979; -
 CC DR INTERPRO: IPR001368; -
 CC DR PROSITE: PS00652; TNFR_C6; 4.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 CC DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 CC KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 CC FT SIGNAL 1 30
 CC FT CHAIN 31 435
 CC FT DOMAIN 31 227
 CC FT TRANSMEM 228 248
 CC FT DOMAIN 249 435
 CC FT REPEAT 42 211
 CC FT REPEAT 82 124
 CC FT REPEAT 125 168
 CC FT REPEAT 169 211
 CC FT REPEAT 43 58
 CC FT DISULFID 59 72
 CC FT DISULFID 62 80
 CC FT DISULFID 83 98
 CC FT DISULFID 101 116
 CC FT DISULFID 104 124
 CC FT DISULFID 126 132
 CC FT DISULFID 139 148
 CC FT DISULFID 142 167
 CC FT DISULFID 170 185
 CC FT CARBOHYD 40 40
 CC FT CARBOHYD 177 177
 CC SQ SEQUENCE 435 AA; 46709 MW; 62462656022F656F CRC64;

Query Match 11.2%; Score 244; DB 1; Length 435;
 Best Local Similarity: 26.9%; Pred. No. 1.8e-10;
 Matches 54; Conservative 32; Mismatches 93; Indels 22; Gaps 6;

QY 9 LVLVDLIIETWTOETLPP-----KYLHPETGHLQCDKCAPSTYKONCTVR 57
 DB 18 VLGLFGLAASQFQAVPVASQENQCRDQKEYEPG--HRICSSRCPPTYSAKCSRI 75
 QY 58 RKLVCPCPHSTDSMHTSDQCVYSPVCKELOSVAQ--ECNRTHRVCECEGR--- 112
 DB 76 RDIVCATCANSENHNNYLLTICQLCP--CDPVAGLEIAPCTSKRTQCCPGMCAA 134
 QY 113 --LEIEFCLHRSQCPGS--GVQAGTPEERTVCKKCPDGFSGSTSKAPCIKHTNSTF 169
 DB 135 WALECHCELLSCPPETELEKDEVGKNNKVCPCAGFQNTSPSACQPHTRCENQ 194
 QY 170 GLLLIOGNATHDNCVSGNRE 190
 DB 195 GLVEAAPGTASDTCCKNPLE 215

RESULT 6
 ID VT2_SFVKA STANDARD; PRT; 325 AA.
 AC P25943;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN 12.
 OS Shope fibroma virus (strain Kasza) (SFV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87321103.
 RA Upton C., Pelange A.M., McFadden G.;
 RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
 RT telomeric region of the Shope fibroma virus genome."
 RL Virology 160:20-30(1987).
 RN (2)
 RP FUNCTION.
 RX MEDLINE: 91207415.
 RA Smith C.A., Davis T., Wagnall J.M., Din W.S., Farrah T., Upton C.,
 RA McFadden G., Goodwin R.G.;
 RT T2 open reading frame from the Shope fibroma virus encodes a soluble
 RT form of the TNF receptor."
 RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
 CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 CC REACH CELLULAR TARGET AND THEREBY DEAMPEINING THE POTENTIAL
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC
 CC EMBL: M17433; -; NOT ANNOTATED_CDS.
 CC DR EMBL: A23727; CA01687.1; -
 CC DR PIR: B43692; B43692.
 CC DR HSSP: P19438; 1TNR.
 CC DR INTERPRO: IPR001368; -
 CC DR PEAM: PF00020; TNFR_C6; 2.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 CC DR PROSITE: PS00650; TNFR_NGFR_2; 1.
 CC KW Receptor; Glycoprotein; Repeat; Signal.
 CC FT SIGNAL 1 16
 CC FT CHAIN 17 325
 CC FT DOMAIN 27 186
 CC FT REPEAT 27 62
 CC FT REPEAT 63 104
 CC FT REPEAT 105 147
 CC FT REPEAT 148 186
 CC FT CARBOHYD 105 105
 CC FT CARBOHYD 181 181
 CC FT CARBOHYD 205 205
 CC FT CARBOHYD 238 238
 CC SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 10.7%; Score 231.5; DB 1; Length 325;
 Best Local Similarity 31.7%; Pred. No. 7e-10;

Matches 59; Conservative 19; Mismatches 91; Indels 17; Gaps 5;
 QY 36 GHQ-----LLCDKADGTLYKOHCTVRRRTLCVPCPDHSYTDMSHTSDQCVYSPCKEL 90
 DB 30 GHDYKDGGLCCASCHPGFYASRLCGSGNTVCSPCEDGTFTASTNHAAPACVSCRGCTGH 89
 QY 91 QSVKQECNTHNRYVCECTTCRYLIEF-----FLKLRHSCPGSGGVQAGTPEERNVCKK 144

Db 90 LSESGPCDRHTRCNCSTGNVYCLLKNGNCRICAPQKCKAGVG-VSGHNRADDTLCEK 148
Qy 145 CPDGFSGEISSKAPCIKHNKSTFGLLLIOGNATHDNCNREATQKCGIDVTL--- 201
Db 149 CPPTATSDLSPTBRCGTSFNYSVGFNLTPV-NETSCCTTAGHNEVTKTEFTVTLNVT 207
Qy 202 -CEAF 206
Db 208 DCDPVE 213

RESULT 7
CD40_BOVIN STANDARD; PRT; 269 AA.
ID CD40_BOVIN
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN TNFRSF5 OR CD40.
OC Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97281252.
RA Hiranio A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle".
RL Immunology 90:294-300(1997).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC EMBL; U57745; AAC48710.1; -
DR HSSP; P25942; 1CDF.
DR INTERPRO: IPR001368; -
DR PFAM; PF00020; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
GN Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 >269 POTENTIAL.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 187 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 746903F30F95F387 CRC64;

Query Match 10.5%; Score 228; DB 1; Length 269;
Best Local Similarity 31.9%; Pred. No. 1.4e-05;
Matches 60; Conservative 21; Mismatches 89; Indels 18; Gaps 5;

29 LHYDPETG-----HQLLDCKAPGTYLKQCTVRRKTLCPVCPDPSHYDTSWHTSDEC 80

Db 18 VHSPEATAGECKQYPPVNSLCDLCPGQKLVNDCTEVSKEGSCGGEPLSTWNEKCY 77
Qy 81 ---VYCSF-VCKELQSVKQECNRTNHNVCCEGGRLL---EIFCLKHNSCPGSGVYA 133
Db 78 HENHYCNPNGLRIOS---EGTLNTDTCVCEGHOHSHTCSCCTPHSCLCLGFGVKQI 134
Qy 134 GTPERNVCKKCPDGFSGEISSKAPCIKHNKSTFGLLLIOGNATHDNCNREATQ 193
Db 135 ATGLDTCVCEPCLGFGFSNVSAPEKCHRWTSCKERGLVQHVGYNKTDVCCFQSMRT 194
Qy 194 KCGIDVTL 201
Db 195 LVYIAPVTM 202

RESULT 8
VT2_MXYVL STANDARD; PRT; 326 AA.
ID VT2_MXYVL
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OC Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9133768.
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence".
RL Virology 184:370-382(1991).
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPEING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC or send an email to license@isb-sib.ch).
CC EMBL; M35181; AAA46632.1; -
DR EMBL; A23726; CA01688.1; -
DR PIR; A40566; GOVZML.
DR HSSP; P19438; ITNR.
DR INTERPRO: IPR001368; -
DR PFAM; PF00020; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
GN Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 326
FT DOMAIN 27 186 4 X TNFR-CYS.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35208 MM; ABBF027E947292FF CRC64;

Query Match 10.1%; Score 220; DB 1; Length 326;

MD: 104875; LTRR.
 DR INTERPRO: IPR001368; .
 DR PFM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT DOMAIN 31 223
 FT TRANSSEM 224 244
 FT DOMAIN 245 415
 FT DOMAIN 42 213
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AEF661 CRC64;

Query Match 9.5%; Score 206; DB 1; Length 415;
 Best Local Similarity 26.1%; Pred. No. 8.5e-08;
 Matches 53; Conservative 32; Mismatches 94; Indels 24; Gaps 8;
 QY 9 LVLVDIIEMTQETLPKRYL-----HYDPETHGLLDCKAPGTYLKQHCYR 57
 DB 18 LILGSLGLVVASQPLVPPRIENGTQMDQKEYEPM--HDVCCSRCPGEVFAVCSRS 75
 QY 58 KRLICVPPDHSYDTSMTSDSCVYCSFYKELQSVKQ--EENRHNHVCDEEER---Y 112
 DB 76 QDVCYKTPHNSYNHNMWHLSTQCLCRP-CDIVLGFEEVAPCTSDRKAECRCQPMSCVY 134
 QY 113 LEIE--FELKRR--SCPPGS--GVVAGTPERTVYCKCPDGFSESTSKAPCIKHTNS 167
 DB 135 LDNECVHEEERLVLCQGTAEVTDDEIMQDVNCPKPGHFOHTSSPRANCPHTICE 194
 QY 168 TFGLLLIQGNATHDNCVSGNRE 190
 DB 195 IQGLVEAPGTSYSDTICKNPPE 217

RESULT 11
 NGFR_HUMAN
 ID NGFR_HUMAN STANDARD; PRT; 427 AA.
 AC P08138;
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-NGFR) (P75 ICD).
 GN NGFR OR TNFRSF16.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87051725.
 RA Johnson D., Lanahan A., Buck C.R., Sehgal A., Morjan C., Mercer E.,
 RA Bothwell M., Chao M.;
 RT "Expression and structure of the human NGF receptor";
 RL Cell 47:545-554(1986).
 RN [2]

RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE; 89069903.
 RA Sehgal A., Patel N., Chao M.;
 RT "A constitutive promoter directs expression of the nerve growth factor
 RT receptor gene";
 RL Mol. Cell. Biol. 8:3160-3167(1988).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC -----
 DR EMBL; M4764; AAB59544.1; .
 DR EMBL; M21621; AAA36363.1; .
 DR PIR; A25218; GQHUN.
 DR HSP; P07174; INGR.
 DR MIM; 162010; .
 DR INTERPRO: IPR000488; .
 DR INTERPRO: IPR001368; .
 DR PFM: PF00020; TNFR_C6; 4.
 DR PFM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 KW Phosphorylation; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 427
 FT DOMAIN 29 250
 FT TRANSSEM 251 272
 FT DOMAIN 273 427
 FT DOMAIN 31 189
 FT REPEAT 31 65
 FT REPEAT 66 107
 FT REPEAT 108 147
 FT REPEAT 148 189
 FT DOMAIN 344 421
 FT DISULFID 32 43
 FT DISULFID 44 57
 FT DISULFID 47 64
 FT DISULFID 67 83
 FT DISULFID 86 99
 FT DISULFID 89 107
 FT DISULFID 109 122
 FT DISULFID 125 138
 FT DISULFID 128 146
 FT DISULFID 149 164
 FT DISULFID 167 180
 FT DISULFID 170 188
 FT DOMAIN 197 248
 FT CARBOHYD 60 60
 SQ SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64;

Query Match 9.1%; Score 199; DB 1; Length 427;
 Best Local Similarity 31.7%; Pred. No. 2.8e-07;
 Matches 52; Conservative 25; Mismatches 71; Indels 16; Gaps 6;
 QY 9 LVLVDIIEMTQETLPKRYLHYDPETHGLLDCKAPGTYLKQHCYRRTLCVPCPD 68
 DB 17 LILGSLGLGAKKACAPGTYLTHSGE-----CKRKNLGEVAPPCA-NQTVCEPCIDS 70

QY 69 -SYTDSMHTSDECVYSPVCKELQSVKQECNRTNHNRYCEEGRYLE-----IEFCLAKR 122
 DB 71 VTFSDVVSATPEPKPCTE-CVGLQSMAPCEVADAVCRAYGYDEDTGCEAC---R 126
 QY 123 SCPGSGVQAGTPERNYVCKKCPDGFSGETSSKAPCIHTNHC 166
 DB 127 VCEAGSGLVFSCODKONTVCEBCPDGTYSDEANHVDPCLPCTYC 170

RESULT 12
 NGFR_RAT
 ID NGFR_RAT STANDARD: PRT: 425 AA.
 AC P07174;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DT LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 (GP80-LNGFR) (P75 ICD).
 NGFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87115859.
 RA Radde M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
 RT "Gene transfer and molecular cloning of the rat nerve growth factor
 RT receptor.";
 RL Nature 325:593-597(1987).
 RN [2]
 RP SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 93077038.
 RA Metis M., Timusk T., Allikmets R., Saarna M., Persson H.;
 RT "Regulatory elements and transcriptional regulation by testosterone
 RT and retinoic acid of the rat nerve growth factor receptor promoter.";
 RL Gene 121:247-254(1992).
 RN [3]
 RP STRUCTURE BY NMR OF 334-418.
 RX MEDLINE: 97449145.
 RA Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
 RL EMBO J 16:4999-5005(1997).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC
 DR EMBL: X05137; CA28763.1;
 DR EMBL: X61269; NOT_ANNOTATED.CDS.
 DR PIR: A26431; A26431.
 DR PDB: INGR; 29-JUL-97.
 DR INTERPRO: IPR000488;
 DR INTERPRO: IPR001368;
 DR PFAM: PF000020; TNFR_C6; 4.
 DR PFAM: PF00531; death_1;
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00500; TNFR_NGFR_2; 4.
 DR PROSITE: PS00117; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;

KW Phosphorylation; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 425
 FT DOMAIN 30 251
 FT TRANSMEM 252 273
 FT DOMAIN 274 425
 FT DOMAIN 32 190
 FT REPEAT 32 66
 FT REPEAT 67 108
 FT REPEAT 109 148
 FT REPEAT 149 190
 FT DOMAIN 198 249
 FT DOMAIN 354 419
 FT DISULFID 33 44
 FT DISULFID 45 58
 FT DISULFID 48 65
 FT DISULFID 68 84
 FT DISULFID 87 100
 FT DISULFID 90 108
 FT DISULFID 110 123
 FT DISULFID 126 139
 FT DISULFID 129 147
 FT DISULFID 150 165
 FT DISULFID 168 181
 FT DISULFID 171 189
 FT CARBOHYD 61 71
 FT CARBOHYD 71 91
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D948327F8 CRC64;

Query Match 9.1%; Score 197.5; DB 1; Length 425;
 Best Local Similarity 22.1%; Pred. No. 3.5e-07;
 Matches 95; Conservative 59; Mismatches 152; Indels 123; Gaps 19;

QY 9 LTVLLDIIEHTQETLPKYLHNDPETHQLDCKAPGYLKHQCTVRRKTLVCPDHP 68
 DB 18 LTLILGVSSGAKETSTGLYHSGE-----CKKCNLGEVQAPGCA-NQYCEFCIDN 71
 QY 69 -SYTDSMHTSDECVYSPVCKELQSVKQECNRTNHNRYCEEGRYLEIE--FCLKHSRCP 125
 DB 72 VTFSDVVSATPEPKPCTE-CLGLQSMAPCEVADAVCRAYGYDEDTGCEACSVCL 130
 QY 126 PGSGVQAGTPERNYVCKKCPDGFSGETSSKAPCIHTNHCIFGLLLQKGNATDNC 185
 DB 131 VGSGLVFSODKONTVCEBCPDGTYSDEANHVDPCLPCTVCEDETEROL----- 178
 QY 186 SGNREATOKGIDVTLCCEAFRF-----AVPTK--IIPNMLSVL 223
 DB 179 ---RECT--NADAE---CEELPGMWRSTPPESDSTAFTSTOPEVPPEDOLVPSYADM 232
 QY 224 VDSLPTKVAESVERIKRRHSQE-----QTOLLKLMK--HONRDOE 265
 DB 233 VTFVVG-----SSQVTVRGTNDNLIPVCSILAAVVVGLVAYIAFKRNSCKOKQCA 286
 QY 266 MVAKTIQ-----DIDLCSSVQRHGHNSLITEQLA--LMESLPKCK-- 306
 DB 287 NSRPVQCTPPPEGEKLSHDSGISVDSOSLHDQTHQTASGALKGDGNLYSLPLTKRE 346
 QY 307 -----ISPEIER--TRTKCKSSEOLKTLISLRINKDGD--TLKG 344
 DB 347 EVELKNGDTWRHLAAGELGYQPEHIDSTFTHAC---PYRALLASH---GAQDSATLDA 398
 QY 345 LMTALKHLK 353
 DB 399 LLAALRRIQ 407

RESULT 13
 FASA_BOVIN
 ID FASA_BOVIN STANDARD: PRT: 323 AA.
 AC P51867;
 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96226401.
 RA Yoo J., Stone R.T., Beattie C.W.;
 RT "Cloning and characterization of the bovine Fas.",
 RL DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
 CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
 CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC
 CC EMBL: U34794; AAC48546.1; -
 CC HSP: P25445; IDPF.
 DR HSP: P25445; IDPF.
 DR INTERPRO: IPR000486; -
 DR INTERPRO: IPR001368; -
 DR PFAM: PF000520; TNFR_c6; 3.
 DR PFAM: PF000531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1
 FT CHAIN 17 323
 FT DOMAIN 17 170
 FT TRANSMEM 171 188
 FT TRANSMEM 189 323
 FT DOMAIN 189 323
 FT DOMAIN 45 163
 FT REPEAT 45 80
 FT REPEAT 81 124
 FT REPEAT 125 163
 FT REPEAT 163 306
 FT DOMAIN 238 306
 FT DOMAIN 306 364
 FT SEQUENCE 323 AA; 36445 MW; 4D88A903E9E1A4892 CRC64;

Query Match 8.7%; Score 190.5; DB 1; Length 323;
 Best Local Similarity 25.6%; Pred. No. 8.1e-07;
 Matches 77; Conservative 37; Mismatches 108; Indels 79; Gaps 18;

Oy 37 HQLADKCAPETYLKQHTVRRKT-LCPYCPD-HSYDTSMTSDECVYCSVCKELQ--S 92
 Db 53 HQFCOPCPPEPKRRKNGDKRDGTPCEVLCSEGEYETDKSHSDKICRS-ICDEHGLE 111
 Oy 93 VKQSCNFRHNVCCEDEERYLEIEFCLKHSRCPGS-----GVVQAGTERTVCKKCDG 148
 Db 112 VEQNCRTNRNCKRKSNFPCSSPC---EHCNPTCTGHEGIIIEKCTPTNCKCK----- 163

Oy 149 FFSGETSKAPCIKHTNCSFGLLI-----QKGNATHD--NVSGNREAR 192
 Db 164 ---GSR-----HAN-SLMALLIDPIVLIYYKVRERKKNNDYCNASASNDGR 212
 Oy 193 QKCIDVTLCEAEFFRAVPTKIIPNMLSYVDSLPSTK---VNASVERIK----- 241
 Db 213 QLNLTVDVL-----GKYIPS---IAEQRITEVKEFVRKNGMEAKIDIDIMHD 257
 Oy 242 RRHSSQECTPOLKLM--KNQND-----QEWKTIORI-DLCESSVGRHLSMLTT 292
 Db 258 NVHETAEQVOLLRNWYQSHGKNAYCTLTLSPLKALAEKIDIVMDITNERENANLN 317
 Oy 293 E 293
 Db 318 E 318
 RESULT 14
 NGFR_CHICK STANDARD; PRT; 416 AA.
 AC P18519;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LNGFR) (P75 ICD).
 GN NGFR.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 90166579.
 RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
 RA Shooter E.M., Reichardt L.F.;
 RT "Structure and developmental expression of the nerve growth factor
 RT receptor in the chicken central nervous system."
 RL Neuron 2:1123-1134(1989).
 RU (2)
 RN
 RP SEQUENCE OF 21-416 FROM N.A.
 RX MEDLINE; 90152140.
 RA Heuer J.G., Fatemie-Najini S., Wheeler E.F., Bothwell M.;
 RT "Structure and developmental expression of the chicken NGF receptor."
 RL Dev. Biol. 137:287-304(1990).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC PIR: JN0006; JN0006.
 DR PIR: A60504; A60504.
 DR HSP: P07174; INGR.
 DR INTERPRO: IPR000488; -
 DR INTERPRO: IPR001368; -
 DR PFAM: PF000520; TNFR_c6; 4.
 DR PFAM: PF000531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 KW Phosphorylation; Signal.
 FT SIGNAL 1
 FT CHAIN 20 416
 FT SIGNAL 19
 FT DOMAIN 29 239
 FT TRANSMEM 240 261
 FT DOMAIN 262 416
 FT DOMAIN 23 181
 FT DOMAIN 23 181

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FT REPEAT 23 57 TNFR-CYS 1.
FT REPEAT 58 100 TNFR-CYS 2.
FT REPEAT 101 140 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT DOMAIN 188 236 SER/THR-RICH.
FT DOMAIN 333 410 DEATH DOMAIN.
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 39 56 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 78 91 BY SIMILARITY.
FT DISULFID 81 99 BY SIMILARITY.
FT DISULFID 101 114 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 120 138 BY SIMILARITY.
FT DISULFID 141 156 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 162 180 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 36 36 C -> Y (IN REF. 2).
FT CONFLICT 173 173 T -> K (IN REF. 2).
FT CONFLICT 276 276 N -> S (IN REF. 2).
FT CONFLICT 396 396 K -> R (IN REF. 2).
SQ SEQUENCE 416 AA; 44654 MM; 68CEAAB54F4D2D56 CRC64;

Query Match 8.48; Score 184; DB 1; Length 416;
Best Local Similarity 30.98; Pred. No. 3.2e-06;
Matches 46; Conservative 28; Mismatches 67; Indels 8; Gaps 6;

OY 41 CDCAPGTYLHOGCTVRKRTLCVPCPDH-SYTDWHTSDCEYVCSPVCKELOSVMQECNR 99
DB 36 CKACNLGEGVQPCGV-NQTVCEPCLDSVTSYDVSATPEKPCPTQ-CVGLHSMAPCPE 93
OY 100 TNHRYCECEBGRYLEIEF---CLKHRSCPPSGVYQAGTPERNYCKKCPDGFESGETSS 156
DB 94 SDAVRCRCAYG-YFGDELSSGCKECSICEVGLGLFPCRDSDYTCCECSPEGTSDANF 152
OY 157 KAPCIKHTNCSTFGILLIQGNATHDNCV 185
DB 153 VDPCLPCTICEE-NEVWKECTATSDAEC 180

RESULT 15
FASL_HUMAN STANDARD; PRT; 335 AA.
P25445;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95 ANTIGEN).
GN TNFRSF6 OR APT1 OR FAS OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91309137.
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA Sameshima M., Hase A., Seto Y., Nagata S.;
RA "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis."
RL Cell 66:233-243(1991).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 226-240; 269-291 AND 321-335.
RX MEDLINE; 92268122.
RA Oehm A., Behnmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
RA Kraemer P.H.;
RA "Purification and molecular cloning of the Apo-1 cell surface
RT antigen, a member of the tumor necrosis factor/nerve growth factor
RT receptor superfamily. Sequence identity with the Fas antigen."

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RL J. Biol. Chem. 267:10709-10715(1992).
RN [3]
RP STRUCTURE BY: NMR OF 218-335.
RX MEDLINE; 97122332.
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.N.;
RT "NMR structure and mutagenesis of the Fas (Apo-1/CD95) death domain."
RL Nature 384:638-641(1996).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD95 entry;
CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROV/CD/CD95.HTM".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M67454; AAA63174.1; -
DR EMBL; X63717; CAA45250.1; -
DR PIR; A40036; A40036.
DR PIR; S24543; S24543.
DR PDB; 1DDF; 12-NOV-97.
DR MIM; 134637; -
DR INTERPRO; IPR000488; -
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_C6; 2.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR.1; 2.
DR PROSITE; PS50050; TNFR_NGFR.2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR KMW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
RW 3D-structure.
FT SIGNAL 1 16
FT CHAIN 17 335
FT DOMAIN 17 173
FT TRANSSEM 174 190
FT TRANSSEM 191 335
FT DOMAIN 47 166
FT DOMAIN 47 83
FT REPEAT 84 127
FT REPEAT 128 166
FT REPEAT 230 314
FT DOMAIN 118 118
FT CARBOHYD 136 136
FT CARBOHYD 136 136
SQ SEQUENCE 335 AA; 37732 MM; 0139942535111410 CRC64;

Query Match 8.48; Score 182; DB 1; Length 335;
Best Local Similarity 25.58; Pred. No. 3.4e-06;
Matches 76; Conservative 34; Mismatches 114; Indels 74; Gaps 15;

OY 19 TQOETLPKXYHYHPERGHOLZCKACAPGYLKHCHYR-RKTCVYCPD-HSTYDSMHT 76
DB 42 TTVETQNLGEGHGOQCHK---PCPEGERKADCTVNGVEPCVQCEKEETTDRAHF 97
OY 77 SDEYVCSPVCKELOSVMQ---CNRTNRYCECEBGRYLEIEFCLKHRSCPPSGGVQAG 134
DB 98 SSKRCRCR-LCDEGHGCAEINCRTNTKRCRCRNPFCNSTVC---EHCPD----- 145

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XX Boyle WJ, Calzone FJ, Lacey DL, Chang MS;
 XX WPI: 1997-334271/31.
 DR N-PSDB; T96062.
 DR
 XX
 XX
 PT Nucleic acid encoding osteoprotegerin - useful for treatment of
 PT diseases involving excessive bone loss, e.g. osteoporosis
 XX
 XX
 PS Claim 23; Pages 106-107; 182pp; German.
 XX
 XX The present sequence is mouse osteoprotegerin (OPG). Anti-OPG
 CC antibodies can be used in OPG diagnostic assays, and as affinity
 CC purification materials. The OPG cDNA can be used to express
 CC recombinant OPG and to generate transgenic animals. It can also
 CC be used to regulate the level of OPG in mammals, specifically to
 CC increase OPG levels, however the use of antisense sequences is
 CC also contemplated. Fragments of the cDNA can be used as probes to
 CC detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or
 CC prevent bone diseases, specifically excessive bone loss, e.g.
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopoenia.
 CC
 SO Sequence 401 AA:

Query Match 100.0%; Score 2179; DB 18; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2,1e-179;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKKWLCALVLDITTEWTOETLPKYLHYDPETHGOLCDKCAPGYLKHCHTVRRKT 60
 DB 1 mkkwlcallylditewttgetlfpkylyhdpethgllcdkcapgylykhchtrvrrkt 60
 QY 61 LCVPCPDHSYTSWMTSDCYVCSPVCKELQSVKQECNRTNHNRCCEGGRYLEIFCFLK 120
 DB 61 lcvpcpdhsytsdwtsdscyvcspvckelqsvkqecnthnrvceegryyleifcflk 120
 QY 121 HNSCPGSGVAVAGTPERNVCKKCPDGFSGETSAPKICIKHTNCSFGLLLIQGNAT 180
 DB 121 hnsccpgsgvavagtpervntvckkcpdgffsgetsakpicikhtncstfgllliqgnat 180
 QY 121 HNSCPGSGVAVAGTPERNVCKKCPDGFSGETSAPKICIKHTNCSFGLLLIQGNAT 180
 DB 121 hnsccpgsgvavagtpervntvckkcpdgffsgetsakpicikhtncstfgllliqgnat 180
 QY 181 HDNVCSGNREATQKCGIDVTLCEAEFFFAVFTKIIPWLSVLDSPGTRVNAESVERI 240
 DB 181 hdnvcsgnreataqcgidvtlceaeffrfaavtkiipwlsvldslpgtkvnaesveri 240
 QY 241 KRRHSSQEQTFOLKLMKQNRDQEMVKKIIDDICSSVQRHGHNSNLTTEQLALME 300
 DB 241 krrhssqeqtfqlklmkqnrddemvkkiddidicessvqrhghnsnlteqllalme 300
 QY 301 SLPGKKISPEEIERRRTCKSSBQLKLLSLWRKNGDDTLKGLMYALKHLKTSHPFKT 360
 DB 301 slpgkkispeeierrrtkckssbqlkllslwrkngddtlkglmyalkhlktsfprkt 360
 QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMGNQYQSVKISCL 401
 DB 361 vthslrktmrflhsftmyrlyqkflflemgnqyqsvkiscsl 401

RESULT 2
 W38343
 ID W38343 standard; Protein; 401 AA.
 AC W38343;
 XX
 XX 20-APR-1998 (first entry)
 DT
 XX Rat osteoprotegerin.
 DE
 XX Rat; osteoprotegerin; antibody; diagnosis; affinity purification;
 KW

KW recombinant production; transgenic animal; treatment; prevention;
 KW antisense oligonucleotide; probe; detection; screening;
 KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;
 KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastases; periodontal bone loss; bone necrosis;
 KW osteopoenia.
 OS
 XX Rattus sp.
 XX
 XX
 XX DE19654610-A1.
 XX
 XX 26-JUN-1997.
 XX
 XX 20-DEC-1996; 96DE-1054610.
 PF
 XX 03-SEP-1996; 96US-0706945.
 PR 22-DEC-1995; 95US-0577788.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Boyle WJ, Calzone FJ, Lacey DL, Chang MS;
 XX WPI: 1997-334271/31.
 DR N-PSDB; T96061.
 DR
 XX
 XX
 PT Nucleic acid encoding osteoprotegerin - useful for treatment of
 PT diseases involving excessive bone loss, e.g. osteoporosis
 XX
 XX
 PS Claim 23; Pages 102-104; 182pp; German.
 XX
 XX The present sequence is rat osteoprotegerin (OPG). Anti-OPG
 CC antibodies can be used in OPG diagnostic assays, and as affinity
 CC purification materials. The OPG cDNA can be used to express
 CC recombinant OPG and to generate transgenic animals. It can also
 CC be used to regulate the level of OPG in mammals, specifically to
 CC increase OPG levels, however the use of antisense sequences is
 CC also contemplated. Fragments of the cDNA can be used as probes to
 CC detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or
 CC prevent bone diseases, specifically excessive bone loss, e.g.
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopoenia.
 CC
 SO Sequence 401 AA:

Query Match 95.4%; Score 2079; DB 18; Length 401;
 Best Local Similarity 94.5%; Pred. No. 8.5e-171;
 Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 NKKWLCALVLDITTEWTOETLPKYLHYDPETHGOLCDKCAPGYLKHCHTVRRKT 60
 DB 1 mkkwlcallylditewttgetlfpkylyhdpethgllcdkcapgylykhchtrvrrkt 60
 QY 61 LCVPCPDHSYTSWMTSDCYVCSPVCKELQSVKQECNRTNHNRCCEGGRYLEIFCFLK 120
 DB 61 lcvpcpdhsytsdwtsdscyvcspvckelqsvkqecnthnrvceegryyleifcflk 120
 QY 121 HNSCPGSGVAVAGTPERNVCKKCPDGFSGETSAPKICIKHTNCSFGLLLIQGNAT 180
 DB 121 hnsccpgsgvavagtpervntvckkcpdgffsgetsakpicikhtncstfgllliqgnat 180
 QY 181 HDNVCSGNREATQKCGIDVTLCEAEFFFAVFTKIIPWLSVLDSPGTRVNAESVERI 240
 DB 181 hdnvcsgnreataqcgidvtlceaeffrfaavtkiipwlsvldslpgtkvnaesveri 240
 QY 241 KRRHSSQEQTFOLKLMKQNRDQEMVKKIIDDICSSVQRHGHNSNLTTEQLALME 300
 DB 241 krrhssqeqtfqlklmkqnrddemvkkiddidicessvqrhghnsnlteqllalme 300
 QY 301 SLPGKKISPEEIERRRTCKSSBQLKLLSLWRKNGDDTLKGLMYALKHLKTSHPFKT 360
 DB 301 slpgkkispeeierrrtkckssbqlkllslwrkngddtlkglmyalkhlktsfprkt 360

Db 301 slpgktspeiertrtctpseqlklslwrkngddtllkglmalkhkhphkpt 360
 QY 361 VTHSLRKTMRFLHSFTMYRLXOKLFLEMIGNOVOSVKISCL 401
 Db 361 vtbelrktirflhsftmyrlyqklflemignqvsvkisc1 401

RESULT 3
 Y05742
 ID Y05742 standard; protein; 401 AA.

AC Y05742;

DT 19-JUL-1999 (first entry)

DE Tumour necrosis factor receptor TR1.

Tumour necrosis factor receptor; TR1; osteoprotegerin; agonist;
 antagonist; screening; human; cancer; AIDS; Alzheimer's disease;
 inflammation; arthritis; septicemia; autoimmune disease;
 psoriasis; inflammatory bowel disease; transplant rejection;
 graft versus host disease; infection; stroke; ischaemia;
 acute respiratory disease syndrome; restenosis; brain injury;
 bone disease; atherosclerosis; therapy.

OS Homo sapiens.

XX EP911633-A1.

XX 28-APR-1999.

PD 02-OCT-1998; 98EP-0203332.

PR 08-OCT-1997; 97US-0061334.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX McDonnell PC, Young PR, Zou J;

DR WPI; 1999-246560/21.

PT Identifying agonists and antagonists of tumor necrosis factor
 related receptors TR1, TR3 and TR5, and of ligand TL3, useful for
 treatment of cancer, AIDS, Alzheimer's disease, bone disease etc

PT Disclosure; Page 10-12; 23pp; English.

CC The present sequence represents tumour necrosis factor receptor
 (TNFR) TR1, also known as osteoprotegerin. The invention relates
 to TNFR related polypeptides TR1, TR3 and TR5 (see Y05742-44) and
 their ligand TL3 (see Y05745). TR1, TR3, TR5 and TL3 are used in
 CC claimed methods of identifying agonists and antagonists, i.e.
 CC compounds that bind to the receptors or ligand, and which activate
 CC (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or
 CC TL3. A screening kit for identifying agonists, antagonists,
 CC ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or
 CC TL3 polypeptides is provided. The agonists and antagonists are
 CC useful for treatment of chronic and acute inflammation, arthritis,
 CC septicemia, autoimmune disease e.g. inflammatory bowel disease,
 CC psoriasis, transplant rejection, graft versus host disease,
 CC infection, stroke, ischaemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
 CC lymphoproliferative disorders), atherosclerosis and Alzheimer's
 CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.

XX Sequence 401 AA;

Query Match 87.28; Score 1900; DB 20; Length 401;
 Best Local Similarity 85.84; Pred. No. 2; 1e-155;
 Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLADI-LEWTTQETLPKRYLHYDPETHGHLCCRCAGPVTYLOKHCTVRRK 59
 Db 1 mnkllc-1-lvflidslskwtctgefpkxlyhdeetsnqlldcpcpgtylkqncakw 59
 QY 60 TLVCPDPHSDYTSWHTSDCYVCSPVCKEIQVQKQPCNTNHNVCBCEGRYLEIEFCL 119
 Db 60 tlvcpdpdhytswhtsdclyspcvckelqyvkqgcntnhrvceckegryleiefcl 119
 QY 120 KHRSCPPGSGVVOAGPERNVTCKCPDGFSGTSSKAPCIKHTNCSFGLLIQKNA 179
 Db 120 khrcspgpgfvgvqgtpernvtckcpdgffsgtsskacporkhtnsvfgllitqgna 179
 QY 180 THDNVCSGNREAROKCIDVTLCEAFRRFVAPKIIIPMLSVYVDSLPCTKYVAESVER 239
 Db 180 thdnicsgnesstqkcgldvltceeaftfaypklfpnlsvyvdnlpgctkvaesver 239
 QY 240 IKRRHSSCEOTFOLLKLMKQNRDOEWKRIIDIDICSSVVRHLHSNLTTEQLALM 299
 Db 240 ikrrhssceqtfqlklmkqnrkdqdivkklididicssvvrhshantteqlslm 299
 QY 300 ESLPGKRIISPEELERTKTKSSBQLIKLISLRKNGDDTLKGLMYALKHKTSHFPK 359
 Db 300 eslpqkrgvgaediektkackpddqllkllslwrkngddtlkglmhalkshktyfpr 359
 QY 360 TYVHSLRKTMRFLHSFTMYRLXOKLFLEMIGNOVOSVKISCL 401
 Db 360 tvqslrktirflhsftmyrlyqklflemignqvsvkisc1 401

RESULT 4

ID W95030 standard; protein; 401 AA.

AC W95030;

DT 13-MAY-1999 (first entry)

DE Tumour necrosis factor receptor (TNF-R) related polypeptide TR1.

XX Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
 KW inflammation; septicemia; autoimmune disease; transplant rejection;
 KW graft vs. host disease; infection; stroke; ischaemia; brain injury; AIDS;
 KW acute respiratory disease syndrome; restenosis; bone disease; cancer;
 KW atherosclerosis; Alzheimer's disease.

XX Unidentified.

OS EP897114-A2.

PN 17-FEB-1999.

PD 04-JUN-1998; 98EP-0304424.

PR 29-AUG-1997; 97US-0057550.

PR 13-AUG-1997; 97US-0055513.

PR 26-AUG-1997; 97US-0056980.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Brigham-burke MR, Young PR;

DR WPI; 1999-134308/12.

PT Identifying agonists and antagonists to tumour necrosis factor
 receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) -
 PT useful for treating stroke, Alzheimer's disease and AIDS

PS Disclosure; Page 11-12; 18pp; English.

CC The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2

or T14 with a candidate compound in the presence of T1 or TR2; and (b) assessing the ability of the candidate compound to compete with T1 or TR2 binding to T12 or T14. TR and TR agonists and antagonists are useful for treating diseases caused by imbalance of IL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, resection, brain injury, AIDS, bone diseases, cancer, atherosclerosis and Alzheimer's disease. The present sequence represents a TNF-R related polypeptide T1.

Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 20; Length 401;

Best Local Similarity 85.8%; Pred. No. 2.1e-155; Mismatches 29; Indels 2; Gaps 2;

Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

1 MNKWLCAALVLDI-IEMTQETLPKYLHYDEPGHQLCDKCAPGYLKQCTVRRK 59

1 mklilcca-lyfldislkwtgctfpylyhydeesthqlcdkcpptylkqhtakwk 59

60 TLVPCPDHSTDSWHTSDECVYCSVCKELQSVKQECNRTNHNVCCEEGRYLEIEFCL 119

60 tvcapcpdhytldswhtsdeclvcsyckelqyvkqecnrthnvcceegryleiefcl 119

120 KHRSGPSSGVVAGTTPRRNVCCKCPDGFSGTSSKAPCKKHNCSTFGILLIOKNA 179

120 khrcspgfigvvagtprrnvcckcpdgfsgtsskacpckhncstfgilltqkxna 179

180 THDNVSGNREATQCGIDVTLCSEAFRRFAVPTKIIPNMLSVLSDIPGTVAESYER 239

180 thdnicsgnsestqcgidvtlceaeaffrfaupktfpmwslvldnlpgtvnaesyer 239

240 IKRRHSQEQTFOLIKLWKHONRDQEMVKIIOIDICSSVQRLGHNSITTEQLALM 299

240 ikrghsqeqtfqllkllkwhqndqdvkkliididicessvqrlghnsitfegqlrslm 299

300 ESLPEKRTISPEIERTRKTKSSSEOLKLSIMRIKNGDODTLGIMYALKHKLTSHPK 359

300 eslpkrtispeiertrtkssseolklsimrikngdodtlgimalkhsktyhpk 359

360 TVTHSLKRTMRLHSFTMYRLYOKLFLEMIGNOVSVKISCL 401

360 tvtgslkrtirflhsftmyrlyoklflemignovsvkiscsl 401

RESULT 5

W83926

W83926 standard; Protein; 401 AA.

W83926;

01-MAR-1999 (first entry)

Human FTHMA-070 protein.

FTHMA-070; human; neurological disorder; therapy; diagnosis.

OS Homo sapiens.

Key Location/Qualifiers

Peptide 1..21

Protein /label= Sig_peptide

17-APR-1998; 98WO-US07714.

10-OCT-1997; 97US-0062017.
18-APR-1997; 97US-0044746.
(MTLL-) MILLENNIUM BIOTHERAPEUTICS INC.
Holtzman D, McCarthy SA;
MPI: 1999-024021/02.
N-PSDB: V69277.
New isolated human FTHMA-070 and T85 proteins - used to develop products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.
Claim 8; Fig 1; 127pp; English.

This is the amino acid sequence of human FTHMA-070, a novel protein having homology to tumour necrosis factor receptor. The sequence was deduced from that of a cDNA clone (see V69277). Isolated from a cardiac coronary artery smooth muscle cell library. FTHMA-070 nucleic acids and polypeptides of the invention are useful as modulating agents in regulating a variety of cellular processes. They can be used for identifying compounds which bind to or modulate the activity of the polypeptides (claimed). They can also be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics), and methods of treatment (e.g. therapeutic and prophylactic) e.g. for neurological disorders.

Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 20; Length 401;

Best Local Similarity 85.8%; Pred. No. 2.1e-155; Mismatches 29; Indels 2; Gaps 2;

Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

1 MNKWLCAALVLDI-IEMTQETLPKYLHYDEPGHQLCDKCAPGYLKQCTVRRK 59

1 mklilcca-lyfldislkwtgctfpylyhydeesthqlcdkcpptylkqhtakwk 59

60 TLVPCPDHSTDSWHTSDECVYCSVCKELQSVKQECNRTNHNVCCEEGRYLEIEFCL 119

60 tvcapcpdhytldswhtsdeclvcsyckelqyvkqecnrthnvcceegryleiefcl 119

120 KHRSGPSSGVVAGTTPRRNVCCKCPDGFSGTSSKAPCKKHNCSTFGILLIOKNA 179

120 khrcspgfigvvagtprrnvcckcpdgfsgtsskacpckhncstfgilltqkxna 179

180 THDNVSGNREATQCGIDVTLCSEAFRRFAVPTKIIPNMLSVLSDIPGTVAESYER 239

180 thdnicsgnsestqcgidvtlceaeaffrfaupktfpmwslvldnlpgtvnaesyer 239

240 IKRRHSQEQTFOLIKLWKHONRDQEMVKIIOIDICSSVQRLGHNSITTEQLALM 299

240 ikrghsqeqtfqllkllkwhqndqdvkkliididicessvqrlghnsitfegqlrslm 299

300 ESLPEKRTISPEIERTRKTKSSSEOLKLSIMRIKNGDODTLGIMYALKHKLTSHPK 359

300 eslpkrtispeiertrtkssseolklsimrikngdodtlgimalkhsktyhpk 359

360 TVTHSLKRTMRLHSFTMYRLYOKLFLEMIGNOVSVKISCL 401

360 tvtgslkrtirflhsftmyrlyoklflemignovsvkiscsl 401

RESULT 6

R99925

R99925 standard; Protein; 401 AA.

R99925;

22-APR-1997 (first entry)

| XX | Full length osteoclastogenesis inhibitory factor. |
|----|---|
| DE | Full length osteoclastogenesis inhibitory factor. |
| XX | |
| KM | Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; |
| XX | osteoporosis. |
| OS | |
| XX | Homo sapiens. |
| XX | |
| FH | Key |
| FT | Location/Qualifiers |
| FT | 1..21 |
| FT | Peptide |
| FT | /note= "Signal peptide" |
| FT | 22..401 |
| FT | Protein |
| XX | /note= "Mature OCIF, claim 6" |
| XX | |
| PN | MO9626217-A1. |
| XX | |
| PD | 29-AUG-1996. |
| XX | |
| XX | 20-FEB-1996; 96WO-JP00374. |
| XX | |
| PR | 21-JUL-1995; 95JP-0207508. |
| PR | 20-FEB-1995; 95JP-0054977. |
| XX | |
| PA | (SNOW) SNOW BRAND MILK PROD CO LTD. |
| XX | |
| PI | Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T; |
| PI | Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; |
| XX | |
| DR | WPI: 1996-403220/40. |
| DR | N-PSDB: T36685. |
| XX | |
| PT | DNA encoding osteoclastogenesis inhibitory factor protein - useful |
| PT | for bone resorption control, esp. treatment of osteoporosis |
| XX | |
| PS | Disclosure: Page 64-66; 183pp; Japanese. |
| XX | |
| CC | This sequence represents the full length osteoclastogenesis inhibitory |
| CC | factor (OCIF) of the invention. The OCIF has a molecular weight by |
| CC | SDS-PAGE of 60 kD under reducing conditions and 120 kD under non- |
| CC | reducing conditions. The protein is adsorbed onto cation-exchangers |
| CC | or heparin and its activity is lowered after 10 mins at 70 deg.C or |
| CC | 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is |
| CC | useful in the control of bone resorption and therefore in the |
| CC | treatment and prevention of disorders of bone resorption, e.g. |
| CC | osteoporosis. |
| XX | |
| XX | Sequence 401 AA: |
| XX | |
| XX | Query Match 87.0%; Score 1895; DB 17; Length 401; |
| XX | Best Local Similarity 85.6%; Pred. No. 5.6e-155; |
| XX | Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2. |
| QY | 1 MNKWLCCALLVLDI-IEVTFQETLPPKRLHRTDPTGHQLCDKCAPGYLKQHCTVRKK 59 |
| DB | 1 mnnllcca-1vdlldisikwtlqetfpkylhydeetsbqlldckcpfylykqhtactakw 59 |
| QY | 60 TCVCPQPDHSYDSNMTSECVYCSVYCKELOSVKQECRNTNRVCEGEGRYLEIEFCL 119 |
| DB | 60 tvcapqpdhyydaswtstdeclycspvckelqyvqecrntnrvcceqegryleietcl 119 |
| QY | 120 KHRSCPGGSGVVOAGTPENTVCKKCPDPFFSGETSSKAPCIKHTNCSYFGILLIQRGNA 179 |
| DB | 120 khrcscppgsgvvgvqagtpentvckrcpdpdffsnetsskacpckhncsvfgyllltdqkna 179 |
| QY | 180 THDNWCSGKREKATQKCGIDVITLCEBAFFRFAYPTKRIIPWLSYVDSLEGTVMASVVR 239 |
| DB | 180 thdnwcsgrkretqkcgidvltlcebaeffrfayptkriipwlsyvdnlpgtkvmasesvr 239 |
| QY | 240 IKRRHSOQOTFOLKLYKHONRNDQMKKIIOIDDLCSSVQRHGHGNSNLTEOQLAM 299 |
| DB | 240 krrghsqoqtfolklklykhonrdmqkiiioiddlcssvqrhghgnsnlteoqlam 299 |
| XX | IKRGHSQGTCTQILKLYKHQNKDQDIVAKKIQGDDICENSVGRHGHGNSNLTEOQLAM 299 |

| | | | |
|--------|--|--|-----|
| Oy | 300 | ESLPKKKISPEIEIRTRKTKSSSEDLKLLSLMRKNGDDODLKLMLAKLTKTSHPFK | 359 |
| Db | 300 | es:pgkxvgaediektckackpsqdikllslsvrkngdqcdtkslmalnkskcyhfpk | 359 |
| Oy | 360 | TVTHSLRKTMRPLHSFTWRLYQKRLFLEMIGNOVSVKISCL | 401 |
| Db | 360 | tvtslkkktrifrlhsftmkykqkiflemignqvsvkiscsl | 401 |
| RESULT | 7 | | |
| ID | W53239 | standard; Protein; 401 AA. | |
| AC | W53239; | | |
| XX | 15-JUL-1998 | (first entry) | |
| DE | Human OCIF genome DNA protein. | | |
| XX | Human; OCIF; genome; osteoclast; antipyretic; osteoporosis; | | |
| KW | rheumatism; multiple sclerosis. | | |
| XX | Homo sapiens. | | |
| OS | | | |
| Key | Location/Qualifiers | | |
| FT | 1..21 | | |
| FT | /label= signal | | |
| FT | Protein | | |
| FT | 22..401 | | |
| FT | /label= OCIF_Protein | | |
| PN | WO9807840-A1. | | |
| PD | 26-FEB-1998. | | |
| XX | 19-AUG-1997; | 97WO-JP02859. | |
| XX | 19-AUG-1996; | 96JP-0235928. | |
| PA | (SNOW) SNOW BRAND MILK PROD CO LTD. | | |
| PI | Moringa T, Nakagawa N, Yasuda H; | | |
| DR | WPI: 1998-169150/15. | | |
| DR | N-PSDB: Y20768. | | |
| PT | Inhibition of osteoclast formation and/or antipyretic activity - | | |
| PT | useful for, e.g. treating osteoporosis, rheumatism and multiple | | |
| PT | sclerosis | | |
| PS | Claim 4; Page 26-28; 36pp; English. | | |
| XX | The present sequence represents human OCIF genome DNA protein which is | | |
| CC | specifically claimed in the present invention. The present invention | | |
| CC | describes: (i) a method of inhibiting the formation of osteoclasts | | |
| CC | and/or antipyretic proteins, which have the following characteristics: | | |
| CC | (1) Mw determined by SDS-PAGE of approximately 60 kDa under reducing | | |
| CC | conditions, and 60 kDa and 120 kDa under non-reducing conditions; (ii) | | |
| CC | 401 aa sequence (iii) (see W53239); (iii) affinity to cation exchangers | | |
| CC | and heparin; (iv) its osteoclast formation inhibiting activity reduced | | |
| CC | by heating at 70 degrees Celsius for 10 minutes or 56 degrees Celsius | | |
| CC | for 30 minutes; and (v) its antipyretic activity reduced by heating at | | |
| CC | 90 degrees Celsius for 10 minutes; and (2) a method for preparing the | | |
| CC | above proteins. The proteins are useful for, e.g. treatment and | | |
| CC | prevention of osteoporosis, rheumatism or multiple sclerosis; and also | | |
| CC | as antigens for immunological diagnosis of these diseases and disorders. | | |
| XX | Sequence | 401 AA; | |
| XX | Query Match | 87.0%; Score 1895; DB 19; Length 401; | |
| XX | Best Local Similarity | 85.6%; Pred. No. 5.6e-15; | |
| XX | Matches 344; Conservative | 76; Mismatches 30; Indels 2; Gaps 2 | |

QY 1 MNKWLCCALLVLDI-1EWTTOETLPKYLHYDEPETHOILCDKCAPGTLYKHQCTVRRK 59
 CC be used to regulate the level of OPG in mammals, specifically to
 CC increase OPG levels, however the use of antisense sequences is
 CC also contemplated. Fragments of the cDNA can be used as probes to
 CC detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or
 CC prevent bone diseases, specifically excessive bone loss, e.g.
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 120 KHRSCPPGSGVQAGTPERTVCKKCPDGFSGSETSKAPCIKHTNCTFGLLIQKNA 179
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 180 THDNVCSGNREATOKGIDVTLCEAFRFAPVPTKIIIPNMLSVLVDLPKTVNAESVER 239
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 240 IKRRHSSQEQTFOLKLMKHONRDQEWKRIIDIDICSSVORHLGHSNLTTEQLALM 299
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 240 IKRRHSSQEQTFOLKLMKHONRDQEWKRIIDIDICSSVORHLGHSNLTTEQLALM 299
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 300 ESLPGKATSPETIRTKTKSSQDLKLSLMRKNGDDTLGKMLAKHKTSHFPK 359
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 360 TVTSLKRTMRFLSHFTMYRLYOKLFLEMIGNOVSVKISCL 401
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 360 TVTSLKRTMRFLSHFTMYRLYOKLFLEMIGNOVSVKISCL 401
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

RESULT 8
 ID W38345 standard: Protein; 401 AA.
 AC W38345;
 DX 20-APR-1998 (first entry)
 DE Human osteoprotegerin.
 KW Osteoprotegerin; antibody; diagnosis; affinity purification;
 KW recombinant production; transgenic animal; treatment; prevention;
 KW antisense oligonucleotide; probe; detection; screening; human;
 KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;
 KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastases; periodontal bone loss; bone necrosis;
 KW osteopaenia.
 KM Homo sapiens.
 OS DE19654610-A1.
 PD 26-JUN-1997.
 PF 20-DEC-1996; 96DE-1054610.
 PR 03-SEP-1996; 96US-0706945.
 PR 22-DEC-1995; 95US-0577788.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Calzone FJ, Lacey DL, Chang MS;
 XX WPI: 1997-334271/31.
 XX N-PSDB; T96063.
 XX Nucleic acid encoding osteoprotegerin - useful for treatment of
 XX diseases involving excessive bone loss, e.g. osteoporosis
 PS Claim 23; Pages 109-111; 182pp; German.
 CC The present sequence is human osteoprotegerin (OPG). Anti-OPG
 CC antibodies can be used in OPG diagnostic assays, and as affinity
 CC purification materials. The OPG cDNA can be used to express

CC recombinant OPG and to generate transgenic animals. It can also
 CC be used to regulate the level of OPG in mammals, specifically to
 CC increase OPG levels, however the use of antisense sequences is
 CC also contemplated. Fragments of the cDNA can be used as probes to
 CC detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or
 CC prevent bone diseases, specifically excessive bone loss, e.g.
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 1 MNKWLCCALLVLDI-1EWTTOETLPKYLHYDEPETHOILCDKCAPGTLYKHQCTVRRK 59
 CC be used to regulate the level of OPG in mammals, specifically to
 CC increase OPG levels, however the use of antisense sequences is
 CC also contemplated. Fragments of the cDNA can be used as probes to
 CC detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or
 CC prevent bone diseases, specifically excessive bone loss, e.g.
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 120 KHRSCPPGSGVQAGTPERTVCKKCPDGFSGSETSKAPCIKHTNCTFGLLIQKNA 179
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 180 THDNVCSGNREATOKGIDVTLCEAFRFAPVPTKIIIPNMLSVLVDLPKTVNAESVER 239
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 240 IKRRHSSQEQTFOLKLMKHONRDQEWKRIIDIDICSSVORHLGHSNLTTEQLALM 299
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 240 IKRRHSSQEQTFOLKLMKHONRDQEWKRIIDIDICSSVORHLGHSNLTTEQLALM 299
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 300 ESLPGKATSPETIRTKTKSSQDLKLSLMRKNGDDTLGKMLAKHKTSHFPK 359
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 360 TVTSLKRTMRFLSHFTMYRLYOKLFLEMIGNOVSVKISCL 401
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

QY 360 TVTSLKRTMRFLSHFTMYRLYOKLFLEMIGNOVSVKISCL 401
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.

RESULT 9
 ID Y43400 standard: Protein; 401 AA.
 AC Y43400;
 DX 28-JAN-2000 (first entry)
 DE Osteoprotegerin protein sequence.
 KW Osteoprotegerin; OPG; human; cardiovascular disease; occlusion;
 KW calcification; blood vessel; atherosclerosis; medial calcific sclerosis;
 KW Monckeberg's arteriosclerosis; therapy.
 OS Homo sapiens.
 PN WO953942-A1.
 PD 28-OCT-1999.
 PF 21-APR-1999; 99MO-US08793.
 PR 23-APR-1998; 98US-0064832.
 PA (AMGE-) AMGEN INC.

XX
PI Simonet S, Sarosi I;
XX
DR WPI: 2000-013182/01.
DR N-PSDB: 237254.
XX

PT Treating and preventing cardiovascular diseases, especially
XX atherosclerosis and Monckeberg's arteriosclerosis -
XX
PS Claim 9; Page 37-39; 43pp; English.

CC This sequence represents the human osteoprotegerin (OPG). The invention
CC relates to a method of treating or preventing cardiovascular disease by
CC administering OPG. The method can be used to treat and prevent
CC cardiovascular diseases associated with occlusion and calcification of
CC blood vessels, especially atherosclerosis or Monckeberg's
CC arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or
CC prevent cardiovascular diseases provides an alternative to invasive
CC treatments. OPG can be used as a single therapeutic for prevention and
CC treatment of both osteoporosis and cardiovascular diseases.

SO Sequence 401 AA;

Query Match 86.8%; Score 1892; DB 21; Length 401;
Best Local Similarity 85.6%; Pred. No. 1e-154;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;

1 MNKKLCCALLVLDI-IMTTOETLPKYLHYDPETHQLCDKCAPGTYLKOHCTVRRK 59
1 mkkllcca-lvldislkwtqetcpkylhydeesthqlcdkcpptylkqhctakwk 59
60 TLVCPDHSYTDMSWHSDECVYCSPVCKELQSVKQECNRTNRYCECEGRYLEIEFCL 119
60 tlvcpdhsytdmswhsdecvycspvckelqsvkqecnrtnrycecegryleiefcl 119
60 tvcapcdhytdmswhsdeclvcsyckelqyvkqecnrtnrycecegryleiefcl 119
120 KHRSPGSGVYVAGTPEPNTVCKKCPDGFSGEHSKAPCKKHNCSTFGILLIQGNA 179
120 khrscpgsgvyvagtpepntvckkcpdgfsnetskacpckhncsvfgilltqgna 179
120 khrcspgfygvagtpernvckrcpdpffsnetsskacpckhncsvfgilltqgna 179
180 THDNVCSGNREATOKCGIDVTLCEAFRFAVPKRIIPNMLSVLVDSPGKRVNAESVER 239
180 thdnvcsnreatkcgidvtlceafrrfapvkripnmlsvlvdspgkrvnaesver 239
180 thdnicsnsestckgldvtlceafrrfapvkripnmlsvlvdspgknaesver 239
240 IKRRHSSQEQTFOLLKLMKHONRDQEWVKKIIDIDCESSVORHLGHSNLTTEQLALM 299
240 ikrhssqeqtfqllklmwhqkagdvkklididlcensvgrhlghsnltteqlrlm 299
300 ESLGKRTISPEIERKTRCKSSSEQLLKLISMRKNGDOTLKLMAALAKHLKTSHPK 359
300 eslgkrtispeierktrckssseqlklismrkngdotlklmalakhlktshepk 359
300 eslpqkkgvgaedleklackpsdqllkliswrlngdgdtklghmalakhslyhpk 359
360 TVTSHLRKTRFSLHSFTMYRRLYOKLFLEMIGNOVOSKISCL 401
360 tvtslhrtktrfslhsftmyrlyoklflemignovoskiscsl 401
360 tvtsghlkttrfslhsftmyrlyoklflemignovoskiscsl 401

RESULT 10
W57635
ID W57635 standard; Protein; 401 AA.
XX
AC W57635;
XX
DT 27-AUG-1998 (first entry)
XX
DE TRI receptor protein.
XX
KW TRI receptor; tumour necrosis factor receptor-1; TNF-alpha; TNF-beta;
KW inhibitor; tumour growth; tumour necrosis; microorganism infection;
KW cellular differentiation stimulation; ionising radiation; septic shock;
KW anti-viral response; growth regulator; immune response; meningococemia;
KW autoimmune disease; apoptosis; inflammation; cachexia; cerebral malaria;
KW AIDS; therapy.

XX
OS Homo sapiens.
XX
PN WO9812344-A1.
XX
XX 26-MAR-1998.
PD
XX 18-SEP-1996; 96WO-US15003.
PF
XX 18-SEP-1996; 96WO-US15003.
PR
XX 18-SEP-1996; 96WO-US15003.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Fleischmann RD, Greene JM, Ni J;
XX
DR WPI: 1998-217278/19.
DR N-PSDB: V24486.
XX

PT New isolated tumour necrosis factor receptor - useful for developing
PT products for treating, e.g. tumours, auto-immune disease(s), graft
PT rejection, apoptosis or inflammation
PS
PS Claim 13; Fig 1; 11pp; English.

CC This sequence is a tumour necrosis factor receptor-1 (TNF) receptor
CC of the invention. The DNA can be used to produce a recombinant host
CC cell by inserting it into a vector, which is then used to transfect the
CC host cell. The TNF receptor can bind both TNF-alpha and TNF-beta. TNF
CC receptor agonists can be used for inhibition of tumour growth and
CC necrosis of tumours. They can also be used to stimulate cellular
CC differentiation, e.g. T cell, fibroblasts or haematopoietic cell
CC differentiation, may be used to augment TNF's role in the host's defence
CC against microorganisms and prevent related disease. The agonists may
CC also be used to protect against the deleterious effects of ionising
CC radiation produced during a course of radiotherapy, e.g. denaturation of
CC enzymes, lipid peroxidation or DNA damage. The agonists may further be
CC used to mediate an anti-viral response, to regulate growth, to mediate
CC the immune response and to treat immunodeficiencies related to diseases
CC such as HIV. Antagonists to the TNF receptor may be used to treat
CC autoimmune diseases, e.g. graft versus host rejection and allograft
CC rejection, and T cell mediated autoimmune diseases. They may also be used
CC to prevent apoptosis. They may also be used to prevent cytotoxicity and
CC to treat septic shock, meningococemia, inflammation, bacterial
CC infections, cachexia, cerebral malaria or AIDS. The products can also be
CC used for diagnosing the above diseases.

SO Sequence 401 AA;

Query Match 86.8%; Score 1891; DB 19; Length 401;
Best Local Similarity 85.3%; Pred. No. 1.2e-154;
Matches 343; Conservative 27; Mismatches 30; Indels 2; Gaps 2;

1 MNKKLCCALLVLDI-IMTTOETLPKYLHYDPETHQLCDKCAPGTYLKOHCTVRRK 59
1 mkkllcca-lvldislkwtqetcpkylhydeesthqlcdkcpptylkqhctakwk 59
60 TLVCPDHSYTDMSWHSDECVYCSPVCKELQSVKQECNRTNRYCECEGRYLEIEFCL 119
60 tlvcpdhsytdmswhsdecvycspvckelqsvkqecnrtnrycecegryleiefcl 119
60 tvcapcdhytdmswhsdeclvcsyckelqyvkqecnrtnrycecegryleiefcl 119
120 KHRSPGSGVYVAGTPEPNTVCKKCPDGFSGEHSKAPCKKHNCSTFGILLIQGNA 179
120 khrscpgsgvyvagtpepntvckkcpdgfsnetskacpckhncsvfgilltqgna 179
120 khrcspgfygvagtpernvckrcpdpffsnetsskacpckhncsvfgilltqgna 179
180 THDNVCSGNREATOKCGIDVTLCEAFRFAVPKRIIPNMLSVLVDSPGKRVNAESVER 239
180 thdnvcsnreatkcgidvtlceafrrfapvkripnmlsvlvdspgkrvnaesver 239
180 thdnicsnsestckgldvtlceafrrfapvkripnmlsvlvdspgknaesver 239
240 IKRRHSSQEQTFOLLKLMKHONRDQEWVKKIIDIDCESSVORHLGHSNLTTEQLALM 299
240 ikrhssqeqtfqllklmwhqkagdvkklididlcensvgrhlghsnltteqlrlm 299

PS Claim 29; Page 94-96; 183pp; Japanese.

XX This sequence represents a mutated version of the full length
 CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
 CC sequence represents OCIF-C195 in which the 19th Cys residue in the
 CC mature OCIF protein is substituted by Ser. The OCIF of the invention
 CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
 CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
 CC cation-exchangers or heparin and its activity is lowered after 10 mins
 CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
 CC deg.C. OCIF is useful in the control of bone resorption and therefore
 CC in the treatment and prevention of disorders of bone resorption, e.g.
 CC osteoporosis.

XX Sequence 401 AA:

Query Match 86.5%: Score 1885; DB 17; Length 401;

Best Local Similarity 85.3%: Pred. No. 4.1e-154; Mismatches 343; Conservative 26; Indels 2; Gaps 2;

1 MNKWLCAALVLDI-IEWTQETLPKRYLHYDEPTGHLCDKCAPGTYLKQHCYVRK 59
 1 mnnllcca-lyfldisikwtqetfprkylhydeetsqllcdkcpptylkqhtakwk 59
 60 TLVPCPDHSTDSWHTSDECVYCSPVCKELQSVKQECNRTNHRVCEGEGRYLEIEFCL 119
 60 tvcapcpdhstyswhtsdeciycspvckelqsvkqecnrtnhrvceckegryleiefcl 119
 120 KHRSCPGSGVVOAGTEPRNTVCKKCPDGFSGETSSKAPCIKHTNCSFGILLIQGNA 179
 120 khrcspgsgvvoagteprntvckkcpdgfsgetsstkapciikhtncsfgilliqgna 179
 120 khrcspgsgvvoagteprntvckkcpdgfsgetsstkapciikhtncsfgilliqgna 179
 120 khrcspgsgvvoagteprntvckkcpdgfsgetsstkapciikhtncsfgilliqgna 179
 180 THDNVCSGNREATOKGIDVTLCSEAFRRVPTKIIPNMLSVLYDSLPGRVNAESVER 239
 180 thdnvcsgnreatokgidvtlceafrrvptkiipnmlsvlydsldpgrvnaesver 239
 180 thdnvcsgnreatokgidvtlceafrrvptkiipnmlsvlydsldpgrvnaesver 239
 240 IKRRHSSQEOFTOLKMKHONRDOEMVKTIIDIDCESSVORHLGHSNTTTEOLLAM 299
 240 ikrrhssqeoftolkmkhondoevmkttiiodidcessvorhlghsnttteollam 299
 240 ikrrhssqeoftolkmkhondoevmkttiiodidcessvorhlghsnttteollam 299
 240 ikrrhssqeoftolkmkhondoevmkttiiodidcessvorhlghsnttteollam 299
 300 ESLPGKISPEIERTRKTKSSSEQLKLSLWIRKNGDODTLKGLMALKHKTSHPPK 359
 300 eslpgkispeiertrktkssseqlklsllwirknngdodtlkglmalhktshppk 359
 300 eslpgkispeiertrktkssseqlklsllwirknngdodtlkglmalhktshppk 359
 300 eslpgkispeiertrktkssseqlklsllwirknngdodtlkglmalhktshppk 359
 360 TVTSHLKRTRMFLHSFTWRYLQKLFLEMIGNOVSVKISCL 401
 360 tvtshlkrtrmflhsftwrylqkflflemignovsvkiscsl 401
 360 tvtshlkrtrmflhsftwrylqkflflemignovsvkiscsl 401

RESULT *13

R99942 ID R99942 standard; Protein; 399 AA.

XX R99942:

XX 23-APR-1997 (first entry)

XX Mutated OCIF, OCIF-CL.

XX Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;

XX osteoporosis.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..21

XX Protein /note- "Signal peptide"

XX W09626217-A1.

XX 29-AUG-1996.

XX 20-FEB-1996. 96WO-JP00374.
 XX 21-JUL-1995; 95JP-0207508;
 XX 20-FEB-1995; 95JP-0054977.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Hiasashio K, Kobayashi F, Mochizuki S, Morinaga T;

XX Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;

XX WPI: 1996-402320/40.

XX N-PSDB; T33172.

XX Claim 62; Page 117-119; 183pp; Japanese.

XX This sequence represents a mutated version of the full length
 CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
 CC sequence represents OCIF-CL in which amino acids 379-380 of the
 CC mature OCIF protein are deleted. The OCIF of the invention
 CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
 CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
 CC cation-exchangers or heparin and its activity is lowered after 10 mins
 CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
 CC deg.C. OCIF is useful in the control of bone resorption and therefore
 CC in the treatment and prevention of disorders of bone resorption, e.g.
 CC osteoporosis.

XX Sequence 399 AA:

Query Match 86.4%: Score 1882; DB 17; Length 399;

Best Local Similarity 85.5%: Pred. No. 7.3e-154; Mismatches 342; Conservative 26; Mismatches 30; Indels 2; Gaps 2;

1 MNKWLCAALVLDI-IEWTQETLPKRYLHYDEPTGHLCDKCAPGTYLKQHCYVRK 59
 1 mnnllcca-lyfldisikwtqetfprkylhydeetsqllcdkcpptylkqhtakwk 59
 60 TLVPCPDHSTDSWHTSDECVYCSPVCKELQSVKQECNRTNHRVCEGEGRYLEIEFCL 119
 60 tvcapcpdhstyswhtsdeciycspvckelqsvkqecnrtnhrvceckegryleiefcl 119
 120 KHRSCPGSGVVOAGTEPRNTVCKKCPDGFSGETSSKAPCIKHTNCSFGILLIQGNA 179
 120 khrcspgsgvvoagteprntvckkcpdgfsgetsstkapciikhtncsfgilliqgna 179
 120 khrcspgsgvvoagteprntvckkcpdgfsgetsstkapciikhtncsfgilliqgna 179
 120 khrcspgsgvvoagteprntvckkcpdgfsgetsstkapciikhtncsfgilliqgna 179
 180 THDNVCSGNREATOKGIDVTLCSEAFRRVPTKIIPNMLSVLYDSLPGRVNAESVER 239
 180 thdnvcsgnreatokgidvtlceafrrvptkiipnmlsvlydsldpgrvnaesver 239
 180 thdnvcsgnreatokgidvtlceafrrvptkiipnmlsvlydsldpgrvnaesver 239
 240 IKRRHSSQEOFTOLKMKHONRDOEMVKTIIDIDCESSVORHLGHSNTTTEOLLAM 299
 240 ikrrhssqeoftolkmkhondoevmkttiiodidcessvorhlghsnttteollam 299
 240 ikrrhssqeoftolkmkhondoevmkttiiodidcessvorhlghsnttteollam 299
 240 ikrrhssqeoftolkmkhondoevmkttiiodidcessvorhlghsnttteollam 299
 300 ESLPGKISPEIERTRKTKSSSEQLKLSLWIRKNGDODTLKGLMALKHKTSHPPK 359
 300 eslpgkispeiertrktkssseqlklsllwirknngdodtlkglmalhktshppk 359
 300 eslpgkispeiertrktkssseqlklsllwirknngdodtlkglmalhktshppk 359
 300 eslpgkispeiertrktkssseqlklsllwirknngdodtlkglmalhktshppk 359
 360 TVTSHLKRTRMFLHSFTWRYLQKLFLEMIGNOVSVKIS 399
 360 tvtshlkrtrmflhsftwrylqkflflemignovsvkiscsl 399
 360 tvtshlkrtrmflhsftwrylqkflflemignovsvkiscsl 399

RESULT 14.

R99934 ID R99934 standard; Protein; 401 AA.

XX R99934:

```

DT 22-APR-1997 (first entry)
XX Mutated OCIF, OCIF-C22S.
XX Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
XX osteoporosis.
XX Synthetic.
XX OS
XX Key Location/Qualifiers
XX Key 1..21
XX Peptide /note= "Signal peptide"
XX Protein 22..401
XX /note= "Mature OCIF-C22S"
XX Misc-difference 277
XX /label= C22S
XX FT
XX PN WO9626217-A1.
XX PD 29-AUG-1996.
XX 20-FEB-1996; 96WO-JP00374.
PR 21-JUL-1995; 95JP-0207508.
PR 20-FEB-1995; 95JP-0054977.
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
XX Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX MPI: 1996-402320/40.
XX DR N-PSDB; T33164.
XX FT DNA encoding osteoclastogenesis inhibitory factor protein - useful
XX PT for bone resorption control, esp. treatment of osteoporosis
XX PS Claim 38; Page 100-102; 183pp; Japanese.
XX CC This sequence represents a mutated version of the full length
XX CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
XX CC sequence represents OCIF-C22S in which the 22nd Cys residue in the
XX CC mature OCIF protein is substituted by Ser. The OCIF of the invention
XX CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
XX CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
XX CC cation-exchangers or heparin and its activity is lowered after 10 mins
XX CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
XX CC deg.C. OCIF is useful in the control of bone resorption and therefore
XX CC in the treatment and prevention of disorders of bone resorption, e.g.
XX CC osteoporosis.
XX ST Sequence 401 AA:
Query Match 86.3%; Score 1880; DB 17; Length 401;
Best Local Similarity 85.1%; Pred. No. 1,1e-153;
Matches 342; Conservative 26; Mismatches 32; Indels 2; Gaps 2;

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DB 1KRGSSQEQTLKILKHKHqkdIvKk1lqddIdcemsVgrHgnanltfeqlsIm 299
QY 300 ESLPGRKISPERIERTRTCKSSQDLKILSLWRKNGDOPTLKGMLYALHKLKTSHPK 359
DB 300 eslpgrkIvgaediektlkaskpsdqIlnlslwrlknqdgdtlkgImalKshskxyhpk 359
QY 360 TVTHSLRKTMRFLHSFTWRYLYOKLFLEMIGNOVSVKISCL 401
DB 360 tvtgsllkktirflhsftmyklygkIflemIqnvqsvKIscl 401
RESULT 15
R99933 standard; Protein; 401 AA.
AC R99933;
XX 22-APR-1997 (first entry)
XX Mutated OCIF, OCIF-C21S.
XX Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
XX osteoporosis.
XX Synthetic.
XX Key Location/Qualifiers
XX Key 1..21
XX Peptide /note= "Signal peptide"
XX Protein 22..401
XX /note= "Mature OCIF-C21S"
XX Misc-difference 277
XX /label= C21S
XX FT
XX PN WO9626217-A1.
XX PD 29-AUG-1996.
XX 20-FEB-1996; 96WO-JP00374.
PR 21-JUL-1995; 95JP-0207508.
PR 20-FEB-1995; 95JP-0054977.
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
XX Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX MPI: 1996-402320/40.
XX DR N-PSDB; T33163.
XX FT DNA encoding osteoclastogenesis inhibitory factor protein - useful
XX PT for bone resorption control, esp. treatment of osteoporosis
XX PS Claim 35; Page 98-100; 183pp; Japanese.
XX CC This sequence represents a mutated version of the full length
XX CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
XX CC sequence represents OCIF-C21S in which the 21st Cys residue in the
XX CC mature OCIF protein is substituted by Ser. The OCIF of the invention
XX CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
XX CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
XX CC cation-exchangers or heparin and its activity is lowered after 10 mins
XX CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
XX CC deg.C. OCIF is useful in the control of bone resorption and therefore
XX CC in the treatment and prevention of disorders of bone resorption, e.g.
XX CC osteoporosis.
XX ST Sequence 401 AA:
SQ

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:51:29 ; Search time 27.53 Seconds
(without alignments)
244.142 Million cell updates/sec

Title: US-09-389-545-2

Perfect score: 2179
Sequence: 1 MNKMLCCALLVLDIIEWTT.....OKLFLEMIGNOVSKISCL 401

Scoring table:
Gapop 10.0 , Gapext 0.5

Indexed: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCRTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCRTUS1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 2179 | 100.0 | 401 | 3 | US-08-974-022-4 Sequence 4, Appl1 |
| 2 | 2079 | 95.4 | 401 | 3 | US-08-974-022-2 Sequence 2, Appl1 |
| 3 | 1892 | 86.8 | 401 | 3 | US-08-974-022-6 Sequence 6, Appl1 |
| 4 | 424.5 | 19.5 | 300 | 2 | US-08-974-022-6 Sequence 2, Appl1 |
| 5 | 382 | 17.5 | 70 | 3 | US-08-974-022-41 Sequence 41, Appl1 |
| 6 | 314 | 14.4 | 227 | 3 | US-08-974-022-48 Sequence 48, Appl1 |
| 7 | 312 | 14.3 | 461 | 1 | US-08-385-229-2 Sequence 2, Appl1 |
| 8 | 312 | 14.3 | 461 | 2 | US-08-650-000-2 Sequence 2, Appl1 |
| 9 | 312 | 14.3 | 461 | 5 | 5395760-2 Patent No. 5395760 |
| 10 | 312 | 14.3 | 474 | 2 | US-08-650-000-4 Sequence 4, Appl1 |
| 11 | 312 | 14.3 | 474 | 5 | 5395760-4 Patent No. 5395760 |
| 12 | 312 | 14.3 | 486 | 1 | US-08-243-010-1 Sequence 1, Appl1 |
| 13 | 312 | 14.3 | 518 | 1 | US-08-385-229-4 Sequence 4, Appl1 |
| 14 | 301.5 | 13.8 | 655 | 3 | US-08-959-382-2 Sequence 2, Appl1 |
| 15 | 297 | 13.6 | 163 | 2 | US-08-219-237B-5 Sequence 5, Appl1 |
| 16 | 296.5 | 13.6 | 164 | 2 | US-08-232-087A-9 Sequence 9, Appl1 |
| 17 | 279 | 12.8 | 48 | 3 | US-08-974-022-43 Sequence 43, Appl1 |
| 18 | 270 | 12.4 | 197 | 3 | US-08-974-022-49 Sequence 49, Appl1 |
| 19 | 268.5 | 12.3 | 625 | 3 | US-08-996-139-15 Sequence 15, Appl1 |
| 20 | 266.5 | 12.2 | 616 | 3 | US-08-996-139-4 Sequence 4, Appl1 |
| 21 | 265.5 | 12.2 | 651 | 3 | US-08-996-139-6 Sequence 6, Appl1 |
| 22 | 253 | 11.6 | 591 | 3 | US-08-996-139-2 Sequence 2, Appl1 |
| 23 | 250.5 | 11.5 | 162 | 2 | US-08-219-237B-7 Sequence 7, Appl1 |
| 24 | 242.5 | 11.1 | 197 | 2 | US-08-505-606-1 Sequence 1, Appl1 |
| 25 | 233.5 | 10.7 | 325 | 4 | US-08-974-022-47 Sequence 2, Appl1 |
| 26 | 233.5 | 10.7 | 325 | 4 | US-08-974-022-47 Sequence 2, Appl1 |
| 27 | 229.5 | 10.5 | 207 | 3 | US-08-974-022-47 Sequence 47, Appl1 |
| 28 | 226 | 10.4 | 355 | 1 | US-08-292-549-6 Sequence 6, Appl1 |

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| 29 | 220 | 10.1 | 326 | 1 | US-08-292-549-4 | Sequence 4, Appl1 |
| 30 | 220 | 10.1 | 326 | 4 | PCT-US91-02207-4 | Sequence 4, Appl1 |
| 31 | 207 | 9.5 | 283 | 4 | PCT-US96-12374-2 | Sequence 2, Appl1 |
| 32 | 199 | 9.1 | 224 | 3 | US-08-974-022-50 | Sequence 50, Appl1 |
| 33 | 187.5 | 8.6 | 159 | 2 | US-08-232-087A-11 | Sequence 11, Appl1 |
| 34 | 187.5 | 8.6 | 159 | 2 | US-08-219-237B-6 | Sequence 6, Appl1 |
| 35 | 187 | 8.6 | 120 | 3 | US-08-974-022-42 | Sequence 42, Appl1 |
| 36 | 182 | 8.4 | 335 | 2 | US-08-219-237B-2 | Sequence 2, Appl1 |
| 37 | 182 | 8.4 | 335 | 2 | US-08-409-338-1 | Sequence 1, Appl1 |
| 38 | 182 | 8.4 | 335 | 4 | PCT-US95-17083-2 | Sequence 19, Appl1 |
| 39 | 179.5 | 8.2 | 314 | 1 | US-08-444-231-19 | Sequence 2, Appl1 |
| 40 | 179.5 | 8.2 | 314 | 4 | US-08-152-443A-19 | Sequence 4, Appl1 |
| 41 | 179.5 | 8.2 | 314 | 4 | PCT-US95-17083-4 | Sequence 52, Appl1 |
| 42 | 177 | 8.1 | 191 | 3 | US-08-974-022-52 | Sequence 2, Appl1 |
| 43 | 177 | 8.1 | 256 | 4 | US-08-236-918A-6 | Sequence 2, Appl1 |
| 44 | 177 | 8.1 | 256 | 4 | PCT-US96-03965-2 | Sequence 6, Appl1 |
| 45 | 170 | 7.8 | 186 | 1 | US-08-089-458B-6 | Sequence 6, Appl1 |

ALIGNMENTS

RESULT 1
US-08-974-022-4
Sequence 4, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: Amgen Inc.
STREET: 1840 DeWittland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
CLASSIFICATION:
FILING DATE: 12-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-4
Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.6e-196;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MNKMLCCALLVLDIIEWTTQETLPKKYHDPFGHQLCKKCAPGYLKHCHVRRRT 60
DB 1 MNKMLCCALLVLDIIEWTTQETLPKKYHDPFGHQLCKKCAPGYLKHCHVRRRT 60
OY 61 LCPVCPDHSYTDMSHSDPCVYCSPIYCKELQSVKQECNTHNRVCECEGRVLEIEFLCK 120

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Db 61 LCVPCHSYTDSMHTSDECVYCSPVCKELQSVKOECHNRTNHRVCECEBGRYLEIEFCLK 120
QY 121 HRSCEPSSGVVQAGTPERNIVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNAT 180
Db 121 HRSCEPSSGVVQAGTPERNIVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNAT 180
QY 181 HDNVCSSGNREATQCGIDVTLCEEAFFRAVPTKIIPNMLSVLYDSLPGTKVNAESVERI 240
Db 181 HDNVCSSGNREATQCGIDVTLCEEAFFRAVPTKIIPNMLSVLYDSLPGTKVNAESVERI 240
QY 241 KRRHSOQTFQKLKMKHQRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
Db 241 KRRHSOQTFQKLKMKHQRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
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QY 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
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RESULT 2

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US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-2
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Query Match 95.4%; Score 2079; DB 3; Length 401;
Best Local Similarity 94.5%; Pred. No. 1.9e-186;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
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QY 61 LCVPCHSYTDSMHTSDECVYCSPVCKELQSVKOECHNRTNHRVCECEBGRYLEIEFCLK 120
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Db 121 HRSCEPSSGVVQAGTPERNIVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNAT 180
QY 181 HDNVCSSGNREATQCGIDVTLCEEAFFRAVPTKIIPNMLSVLYDSLPGTKVNAESVERI 240
Db 181 HDNVCSSGNREATQCGIDVTLCEEAFFRAVPTKIIPNMLSVLYDSLPGTKVNAESVERI 240
QY 241 KRRHSOQTFQKLKMKHQRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
Db 241 KRRHSOQTFQKLKMKHQRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
QY 301 SLPGKKSPEIEIERTKTKCSSEQLKLLSLMRKNGDQDTLKGMLAKHLKTSHPKPT 360
Db 301 SLPGKKSPEIEIERTKTKCSSEQLKLLSLMRKNGDQDTLKGMLAKHLKTSHPKPT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
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RESULT 3

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US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-6
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Query Match 86.8%; Score 1892; DB 3; Length 401;
Best Local Similarity 85.6%; Pred. No. 5.8e-169;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;
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Qy 60 TLCPVPCDHSYTDWMTSDCYVCCSPVCKELQSVKQCNRTNHNVCCEGREGYLEIFCL 119
Db 60 TVCAPCDHYTDSMHTSDCLVCSPPCKELQYVKQCNRTNHNVCCEGREGYLEIFCL 119
Qy 120 KHSNCPGSSVQAGTERTVCKKCPDGFSSGTSKACIKRTNSTGILLIQGNA 179
Db 120 KHSNCPGSSVQAGTERTVCKKCPDGFSSGTSKACIKRTNSTGILLIQGNA 179
Qy 180 THDVCNREATOKCIGDITLCEAFRRVAPTKIIPNMLSVLVDSLPCKVAESVER 239
Db 180 THDVCNREATOKCIGDITLCEAFRRVAPTKIIPNMLSVLVDSLPCKVAESVER 239
Qy 240 IKRHSSEOETFOLLKLMKHONRQDQVKKIIOIDICSSVORHLGSHNLTQALLM 299
Db 240 IKRHSSEOETFOLLKLMKHONRQDQVKKIIOIDICSSVORHLGSHNLTQALLM 299
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Db 300 ESLPGRKISPEEIERTRKTKSSFOLLKLSMIRKNGDDTLKGLMALKHLSHPK 359
Qy 360 TVTSLKTRMFLHSFTMYRLYOKLFLEMIGNOVQYKISCL 401
Db 360 TVTSLKTRMFLHSFTMYRLYOKLFLEMIGNOVQYKISCL 401

RESULT 4
US-08-794-796-2
Sequence 2, Application US/08794796
Patent No. 5885800
GENERAL INFORMATION:
APPLICANT: Emery, John
APPLICANT: Tan, KB
APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tumor Necrosis Related Receptor.
TITLE OF INVENTION: TR4
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Smithline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
- COMPUTER: IBM Compatible
- OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-794-796-2
Query Match 19.5%; Score 424.5; DB 2; Length 300;
Best Local Similarity 39.0%; Pred. No. 6e-32;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;
Qy 26 PKYLHDPETGHLCDKCAPGTYLKQCHTVRRKTLCPVPCDHSYTDWMTSDCYVCCSP 85
Db 34 PTYPMWDAETGELRYVQAOCPPGTFVQPCRRDSPTCGPDPHRYQFMWYLERCRVCNV 93
Qy 86 VCKELQSVKQCNRTNHNVCCEGREGYLEIFCLIKHSCPPGSSGVQAGTERTVCKKC 145
Db 94 LCGEREERACATNHRACRCRTGFFAHAGFCLERHASCPPGAGVYARPTSPQNTQCP 153
Qy 146 PDGFSGETSSKAPCIKRTNSTGILLIQGNATHDNV--CSGNREATOKCIGDITL 202
Db 154 PGGFSASSSSSQCPQHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVGAEE--C 211
Qy 203 EEAFFRVAPTKIIPNMLSVLVDSL 227
Db 212 ERAVIDFVAPQDISIKRLQRLQAL 236

RESULT 5
US-08-974-022-41
Sequence 41, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Witter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-41

Query Match 17.5%; Score 382; DB 3; Length 70;
Best Local Similarity 94.3%; Pred. No. 7.3e-29;
Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 8 ALLVLDIIMETQETLPKYLHDPETGHLCDKCAPGTYLKQCHTVRRKTLCPVPCD 67

TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-650-000-2

Query Match 14.3%; Score 312; DB 2; Length 461;
Best Local Similarity 34.7%; Pred. No. 3.6e-21;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

QY 8 ALLVLDITLMTQETLPK--YLHYDPETGH-----QLLDCAPGTYLKH 53
DB 9 ALAVGLEL--WAAAHALPAQVAFTPYAPFEGSTCRRLREYIDQTAQMCSCSPQAHKVF 66
QY 54 CTVRRTLCVPCPDHSTYDSMTSDECVYCSPYCKELQSVKQECNRTNHNVCCEEGRYL 113
DB 67 CTKSTDTVCDSCESTYTQIMNWPBELSGSRCSDDQVETQACTRQONICICRPGWC 126
QY 114 EI-----EFLKHSRCPGSGVYQAGTPERNVCKKCPDGFSGETSSKAPCIKHTNCS 167
DB 127 ALKQSGCRCLAPLRKCRPGFGVARGPTEISDVYCKPCAPGTFSSNTSSIDICRPHQICN 186
QY 168 TFGLLIQKGNATHDNCVS 186
DB 187 VVAI-----PGNASMDAVCT 201

RESULT 9
5395760-2

Patent No. 5395760
APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
B-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO: 2
LENGTH: 461
5395760-2

Query Match 14.3%; Score 312; DB 5; Length 461;
Best Local Similarity 34.7%; Pred. No. 3.6e-21;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

QY 8 ALLVLDITLMTQETLPK--YLHYDPETGH-----QLLDCAPGTYLKH 53
DB 9 ALAVGLEL--WAAAHALPAQVAFTPYAPFEGSTCRRLREYIDQTAQMCSCSPQAHKVF 66
QY 54 CTVRRTLCVPCPDHSTYDSMTSDECVYCSPYCKELQSVKQECNRTNHNVCCEEGRYL 113
DB 67 CTKSTDTVCDSCESTYTQIMNWPBELSGSRCSDDQVETQACTRQONICICRPGWC 126
QY 114 EI-----EFLKHSRCPGSGVYQAGTPERNVCKKCPDGFSGETSSKAPCIKHTNCS 167
DB 127 ALKQSGCRCLAPLRKCRPGFGVARGPTEISDVYCKPCAPGTFSSNTSSIDICRPHQICN 186
QY 168 TFGLLIQKGNATHDNCVS 186
DB 187 VVAI-----PGNASMDAVCT 201

RESULT 10
US-08-650-000-4
Sequence 4, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:

APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wight, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-650-000-4

Query Match 14.3%; Score 312; DB 2; Length 474;
Best Local Similarity 34.3%; Pred. No. 3.8e-21;
Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;

QY 5 LCCALLVLDIEMTQETLPKYL--HYDEPTGH-----QLLCKRCAPGT 49
DB 6 LVALVLELQ--WATGTVPAQVLLPYKPEPGYECIOSEYTRKAKQCCACPPGQY 63
QY 50 LKQCHTVRRKTLVCPDHSYDMSHTSDCYCSPYCKELQSVKQECNRTNRYCEEE 109
DB 64 VKHFCNKTSDTVACDCEASMTQVWNOFRICLSSSCTTDQVEIRACTKQNRVCA 123
QY 110 GRYLEIEF-----CLKHSCPPGSGVQAGTPERTVCKKCPDGFSGEITSKAPC 162
DB 124 GRVALKTHSGSCRCQKRLSKCGPGFGVASSRAPNGVNLCKACAPGTFTSDTSC 183
QY 163 HTNCGTFGLLIQKGNATHDNCVCS 186
DB 184 HRICS-----ILAIIPGNASTDAVCA 203

RESULT 11
Patent No. 5395760
APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
B-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO: 4:
LENGTH: 474
5395760-4

Query Match 14.3%; Score 312; DB 5; Length 474;
Best Local Similarity 34.3%; Pred. No. 3.8e-21;

Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;
QY 5 LCCALLVLDIEMTQETLPKYL--HYDEPTGH-----QLLCKRCAPGT 49
DB 6 LVALVLELQ--WATGTVPAQVLLPYKPEPGYECIOSEYTRKAKQCCACPPGQY 63
QY 50 LKQCHTVRRKTLVCPDHSYDMSHTSDCYCSPYCKELQSVKQECNRTNRYCEEE 109
DB 64 VKHFCNKTSDTVACDCEASMTQVWNOFRICLSSSCTTDQVEIRACTKQNRVCA 123
QY 110 GRYLEIEF-----CLKHSCPPGSGVQAGTPERTVCKKCPDGFSGEITSKAPC 162
DB 124 GRVALKTHSGSCRCQKRLSKCGPGFGVASSRAPNGVNLCKACAPGTFTSDTSC 183
QY 163 HTNCGTFGLLIQKGNATHDNCVCS 186
DB 184 HRICS-----ILAIIPGNASTDAVCA 203

RESULT 12
US-08-243-010-1
Sequence 1, Application US/08243010
Patent No. 5639597
GENERAL INFORMATION:
APPLICANT: Laufer, Leander
APPLICANT: Zettlmeissel, Gerd
APPLICANT: Oquendo, Patricia
TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,010
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1132-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 486 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-243-010-1

Query Match 14.3%; Score 312; DB 1; Length 486;
Best Local Similarity 34.7%; Pred. No. 3.9e-21;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;
QY 8 ALVALVLDIEMTQETLPK--YLHYDEPTGH-----QLLCKRCAPGTYLKQ 53

Db 9 ALAVGLEL--WAAAHALPAQVAFITPIAPFEPSTCHLRITYDTQTAMCCSKSPGOHAYF 66
OY 54 CTVRKRLCVPCPDHSTYDTSWHTSDEVCYSPVKELQSVKQECNRTHNRYCEEGRYL 113
Db 67 CTKTSDFVDCSDCESTYQLNMWVPECLSCGRSSDQVEVQACRRENRICTCRPGWYC 126
OY 114 EI-----EFLKHSRCPGSGVVOAGTPEPRNTYCKKCPDGFSGEISKAPCIKHNC 167
Db 127 ALSKQEGRLCAPLRKCRPGFVAPGTETSDVCKPCAPGTFSTNTSTDICRPHOICN 186
OY 168 TFGLLIOLKGNATHDNVCS 186
Db 187 VVAL-----PGNASMDAVCT 201

RESULT 13
US-08-385-229-4
Sequence 4, Application US/08385229
Patent No. 5605690

GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,229
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-385-229-4

Query Match 14.3%; Score 312; DB 1; Length 518;
Best Local Similarity 34.7%; Pred. No. 4.3e-21;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

OY 8 ALVLDIIETWTQETLPPK--YLHYDEPETH-----QLCDKCAPGYLKH 53
Db 38 ALAVGLEL--WAAAHALPAQVAFITPIAPFEPSTCHLRITYDTQTAMCCSKSPGOHAYF 95
OY 54 CTVRKRLCVPCPDHSTYDTSWHTSDEVCYSPVKELQSVKQECNRTHNRYCEEGRYL 113
Db 96 CTKTSDFVDCSDCESTYQLNMWVPECLSCGRSSDQVEVQACRRENRICTCRPGWYC 155

OY 114 EI-----EFLKHSRCPGSGVVOAGTPEPRNTYCKKCPDGFSGEISKAPCIKHNC 167
Db 156 ALSKQEGRLCAPLRKCRPGFVAPGTETSDVCKPCAPGTFSTNTSTDICRPHOICN 215
OY 168 TFGLLIOLKGNATHDNVCS 186
Db 216 VVAL-----PGNASMDAVCT 230

RESULT 14
US-08-959-382-2
Sequence 2, Application US/08959382
Patent No. 6013476

GENERAL INFORMATION:
APPLICANT: DEEN, KEITH
APPLICANT: HURLE, MARK
APPLICANT: YOUNG, PETER
APPLICANT: TAN, K.B.
TITLE OF INVENTION: Tumor Necrosis Related Receptor,
TITLE OF INVENTION: TR7
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,382
FILING DATE: 28-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,796
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169

INFORMATION FOR SPO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-959-382-2

Query Match 13.8%; Score 301.5; DB 3; Length 655;
Best Local Similarity 29.0%; Pred. No. 5.7e-20;
Matches 91; Conservative 40; Mismatches 150; Indels 33; Gaps 7;

OY 10 LVLDIIETWTQETLPPK--YLHYDEPETH-----QLCDKCAPGYLKH 63
Db 30 LLLGLFSTTAAPEKASNLIGYRHVDATGCVLTCDKCAPGYVSEHCTMTSLRVC 89
OY 64 PCPDHSTYDTSWHTSDEVCYSPVKELQSVKQECNRTHNRYCEEGRYL 123
Db 90 SCPVGTETTRHENGIEKCHDSOPCPWPMIEKLPCAALTDRECTCPGPMFSNATCAPHTV 149
OY 124 CPFGSGVVOAGTPEPRNTYCKKCPDGFSGEISKAPCIKHNTSTFLLIOLKGNATHDN 183
Db 150 CPVGMGRKKGITETEDVRKQACAGTSDVPSVMCKAATIDLSLNLVYIKGTKETDN 209

Search completed: December 27, 2000, 10:53:53
Job time: 144 sec

OY 184 VC-----SGNREATOKCGIDVTLCERAFRRFAYPTK-IIPNMLSVLYDSLPKTVNAESVE 238
Db 210 VCGTLPSPSSSTSPSPGTAIFPRPEHMETHEVPSSTYPRKGN-----STESNSSASV 262
OY 229 RIKRRHSSOEOTFOLLKLMKHON---RDQEMVKTIIDIDICESSVQRHLGHSNLTTEQ 294
Db 263 RPKVLSSTIOEGTVP-----DNTSSARKEEDVNTLPMLQYVNNHQGPHHRH----ILK 311
OY 295 LLALMESLPGRKIS 308
Db 312 LLPSMETATGGERKS 325

RESULT 15
US-08-219-237B-5
; Sequence 5, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Helliwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Helliwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-219-237B-5

Query Match 13.6%; Score 297; DB 2; Length 163;
Best Local Similarity 36.8%; Pred. No. 2.1e-20;
Matches 60; Conservative 17; Mismatches 74; Indels 12; Gaps 3;
OY 30 HDPPEGHOLLDKCAPGYTLKQHCVRKRTLCVPCPDHSTYDSMHTSDCYCSPVCKE 89
Db 7 YTDQTA--OMCSCSKSPGQHAKEVCTKTSYDVCSDCEDSTYTQLMNVPECLSCGSRCD 64
OY 90 LOSVROECNRHTNRVCECEGRYLEI-----EFLKHSRSCPPGSGVQAGTPERNTVCK 143
Db 65 DQVETQACRRENRICTCRPGWYCALSKQEGRLCAPLKRCRGFGVAPRGTTSDVYCK 124
OY 144 KCPDGFSETSSKAPCIKHTNCSFTGILLIQQKNAHTHDNVC 186
Db 125 PCAPGTFSNTSTSDICRPHQICNVVAI-----PGNASMDAVCT 163

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: December 27, 2000, 10:52:40 ; Search time 60.82 Seconds
(without alignments)
615.637 Million cell updates/sec

Title: us-09-389-545-8

Sequence: 1 MDKHTPCPPAPAPLLGGPS.....QKGNATHDNCISNSETOK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:REMBL.14:*
2: SP:archaea:*
3: SP:bacteria:*
4: SP:fungi:*
5: SP:human:*
6: SP:invertebrate:*
7: SP:mammal:*
8: SP:mhc:*
9: SP:organelle:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 1009 | 44.9 | 401 | 4 000300 | 000300 homo sapien |
| 2 | 1008 | 44.9 | 372 | 4 09UH94 | 09UH94 homo sapien |
| 3 | 888 | 39.5 | 401 | 11 008712 | 008712 mus musculu |
| 4 | 875 | 39.0 | 401 | 11 008727 | 008727 rattus norv |
| 5 | 824.5 | 36.7 | 437 | 11 09RI44 | 09RI44 mus musculu |
| 6 | 433 | 19.3 | 300 | 4 095407 | 095407 homo sapien |
| 7 | 405.5 | 18.1 | 302 | 13 09PUS0 | 09PUS0 mus musculu |
| 8 | 332.5 | 16.8 | 459 | 11 062327 | 062327 mus musculu |
| 9 | 331 | 16.7 | 439 | 4 016042 | 016042 homo sapien |
| 10 | 327 | 16.6 | 482 | 11 088734 | 088734 mus musculu |
| 11 | 287 | 12.8 | 655 | 4 075509 | 075509 homo sapien |
| 12 | 276 | 12.3 | 384 | 4 09HP60 | 09HP60 homo sapien |
| 13 | 272.5 | 12.1 | 684 | 13 090544 | 090544 ginglymosto |
| 14 | 252.5 | 11.2 | 616 | 4 09T606 | 09T606 homo sapien |
| 15 | 252.5 | 11.2 | 625 | 11 035305 | 035305 mus musculu |
| 16 | 234.5 | 10.4 | 349 | 12 057103 | 057103 monkeypox v |
| 17 | 233.5 | 10.4 | 349 | 12 057099 | 057099 monkeypox v |
| 18 | 231.5 | 10.3 | 349 | 12 057291 | 057291 monkeypox v |
| 19 | 231.5 | 10.3 | 349 | 12 057100 | 057100 monkeypox v |

| | | | | | |
|----|-------|------|-----|-----------|---------------------|
| 20 | 231.5 | 10.3 | 349 | 12 057101 | 057101 monkeypox v |
| 21 | 231.5 | 10.3 | 349 | 12 057102 | 057102 monkeypox v |
| 22 | 230.5 | 10.3 | 348 | 12 057277 | 057277 monkeypox v |
| 23 | 230.5 | 10.3 | 348 | 12 057108 | 057108 monkeypox v |
| 24 | 229 | 10.2 | 348 | 12 057112 | 057112 variola vir |
| 25 | 229 | 10.2 | 348 | 12 085407 | 085407 variola vir |
| 26 | 226.5 | 10.1 | 349 | 12 057284 | 057284 camelipox vl |
| 27 | 226.5 | 10.1 | 349 | 12 057098 | 057098 camelipox vl |
| 28 | 226 | 10.1 | 349 | 12 057110 | 057110 variola vir |
| 29 | 226 | 10.1 | 349 | 12 057111 | 057111 variola vir |
| 30 | 226 | 10.1 | 349 | 12 089118 | 089118 variola vir |
| 31 | 226 | 10.1 | 349 | 12 089098 | 089098 variola vir |
| 32 | 223 | 9.9 | 350 | 12 057116 | 057116 cowpox viru |
| 33 | 222.5 | 9.9 | 349 | 12 057097 | 057097 camelipox vl |
| 34 | 222.5 | 9.9 | 355 | 12 085308 | 085308 cowpox viru |
| 35 | 221 | 9.8 | 349 | 12 057109 | 057109 variola vir |
| 36 | 220.5 | 9.8 | 349 | 12 057305 | 057305 cowpox viru |
| 37 | 217.5 | 9.7 | 326 | 12 057120 | 057120 cowpox viru |
| 38 | 217.5 | 9.7 | 326 | 12 057122 | 057122 cowpox viru |
| 39 | 217.5 | 9.7 | 351 | 12 073559 | 073559 cowpox viru |
| 40 | 217.5 | 9.7 | 360 | 12 057118 | 057118 cowpox viru |
| 41 | 216.5 | 9.6 | 351 | 12 057117 | 057117 cowpox viru |
| 42 | 214.5 | 9.6 | 350 | 12 057123 | 057123 cowpox viru |
| 43 | 212.5 | 9.5 | 347 | 12 057115 | 057115 cowpox viru |
| 44 | 211.5 | 9.4 | 351 | 12 057121 | 057121 cowpox viru |
| 45 | 209.5 | 9.3 | 283 | 4 092956 | 092956 homo sapien |

ALIGNMENTS

RESULT 1
ID 000300 PRELIMINARY: PRT: 401 AA.
AC 000300; 060236;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE OSTEOCYTE-ASSOCIATED PRECURSOR (OSTEOCYTE-ASSOCIATED FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RP TISSUE-KIDNEY.
RX MEDLINE: 97262071.
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luechly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.,
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density." Cell 89:309-319(1997).
[2]
RP SEQUENCE FROM N.A.
RP TISSUE-LUNG FIBROBLAST.
RX MEDLINE: 98151033.
RA Yaşuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.,
RA "Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
osteoclastogenesis in vitro." Endocrinology 139:1329-1337(1998).
[3]
RP SEQUENCE FROM N.A.
RP TISSUE-PLACENTA.
RX MEDLINE: 98351569.
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.,

"Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Eur. J. Biochem. 254:685-691(1998).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AB0082146; BAA32076.1; -.
 DR EMBL: AB008822; BAA32076.1; -.
 DR EMBL: U94332; BAB53709.1; -.
 DR HSP: P25942; ICDF.
 DR MIM: 602643; -.
 DR INTERPRO: IPRO01368; -.
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT DOMAIN 23 183
 FT REPEAT 23 63
 FT REPEAT 64 106
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT DOMAIN 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 98
 FT CARBOHYD 152 152
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT CONFLICT 263 263
 SEQUENCE 401 AA; 45996 MW; EB42PA51C9D7C71E CRC64;

Query Match 44.9%; Score 1009; DB 4; Length 401;
 Best Local Similarity 99.4%; Pred. No. 6.6e-80;
 Matches 173; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 228 KETPPKYLHDEETSHOGLCDKCPGTYLKHOKCTAKKTYCACPDHYTDSMHTSDEC 287
 DB 21 QETPPKYLHDEETSHOGLCDKCPGTYLKHOKCTAKKTYCACPDHYTDSMHTSDEC 80
 QY 288 LYCSVPKELQYVQECNRTNRYVCECKEGRYLEIEFLKHSRCPGPGVYVQAGTPERNV 347
 DB 81 LYCSVPKELQYVQECNRTNRYVCECKEGRYLEIEFLKHSRCPGPGVYVQAGTPERNV 140
 QY 348 VCKRCPDGFSENETSSKAPCKRHTNCSYFGLLTQKGNATHDNCISGNSSESTOK 401
 DB 141 VCKRCPDGFSENETSSKAPCKRHTNCSYFGLLTQKGNATHDNCISGNSSESTOK 194

RESULT 2
 ID Q9UHP4 PRELIMINARY; PRT; 372 AA.
 AC Q9UHP4;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE OSTEOPROTEGERIN (FRAGMENT).
 OS Homo sapiens (human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
 RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
 DR EMBL: AF134187; AAF20168.1; -.
 DR INTERPRO: IPRO01368; -.
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 FT NON_TER 1
 SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 44.9%; Score 1008; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 7.4e-80;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ETPPKYLHDEETSHOGLCDKCPGTYLKHOKCTAKKTYCACPDHYTDSMHTSDECL 288
 DB 1 ETPPKYLHDEETSHOGLCDKCPGTYLKHOKCTAKKTYCACPDHYTDSMHTSDECL 60
 QY 289 YCSVPKELQYVQECNRTNRYVCECKEGRYLEIEFLKHSRCPGPGVYVQAGTPERNV 348
 DB 61 YCSVPKELQYVQECNRTNRYVCECKEGRYLEIEFLKHSRCPGPGVYVQAGTPERNV 120
 QY 349 CKRCPDGFSENETSSKAPCKRHTNCSYFGLLTQKGNATHDNCISGNSSESTOK 401
 DB 121 CKRCPDGFSENETSSKAPCKRHTNCSYFGLLTQKGNATHDNCISGNSSESTOK 173

RESULT 3
 ID 008712 PRELIMINARY; PRT; 401 AA.
 AC 008712; 070202;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).
 GN TNFRSF11B OR OPB.
 OS Mus musculus (mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=KIDNEY;
 RX MEDLINE: 97263071.
 RA Simeonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose E., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
 RT Cell 89:309-319(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/OLA AND NIH SWISS;
 RX MEDLINE: 98382527.
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T., Higashio K.;
 RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";
 RL Gene 215:339-343(1998).

CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
 CC PLACENTA. NOT DETECTED IN SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
 CC 15 TO DAY 17.
 CC -1- SIMILARITY: CONTRAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: U94331; AAB53708.1; -.
 CC EMBL: AB013898; BAA28269.1; -.
 CC EMBL: AB013903; BAA33388.1; -.
 CC EMBL: AB013899; BAA33388.1; JOINED.
 CC EMBL: AB013900; BAA33388.1; JOINED.
 CC EMBL: AB013901; BAA33388.1; JOINED.
 CC EMBL: AB013902; BAA33388.1; JOINED.
 CC HSSP: P25942; ICDF.
 CC MGSP: MGI:109587; OPG.
 CC INTERPRO: IPR000488; -.
 CC INTERPRO: IPR001368; -.
 CC PIRAM: PF00020; TNFR_C6; 3.
 CC PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 CC PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC PROSITE: PS50050; TNFR_NGFR_2; 2.
 CC KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT DOMAIN 23 201
 FT REPEAT 23 201
 FT REPEAT 23 201
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT DOMAIN 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 165
 FT CARBOHYD 178 178
 FT CARBOHYD 178 289
 FT CARBOHYD 138 289
 FT VARIANT 138 289
 FT VARIANT 161 161
 FT VARIANT 165 165
 FT VARIANT 288 288
 FT VARIANT 296 296
 FT SEQUENCE 401 AA; 45923 MW; CAA6102DB312470 CRC64;
 Query Match 39.5%; Score 888; DB 11; Length 401;
 Best Local Similarity 86.8%; Pred. No. 2.2e-69;
 Matches 151; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
 Oy 228 KETFPKYLHYDEETSHOLCDKCPGTYLKHOCFAKMTVCAPCDHYTDSMHTSDSC 287
 Db 21 QETLPKYLHYDEETSHOLCDKCPGTYLKHOCFAKMTVCAPCDHYTDSMHTSDSC 80
 Oy 288 LYCSFVCKELQVYKOCNFTNHNRCVCEKGRYLEIFCLKHRSCEPGFVVOAGTPEPNT 347
 Db 81 VYCSFVCKELQVYKOCNFTNHNRCVCEKGRYLEIFCLKHRSCEPGFVVOAGTPEPNT 140

Oy 348 VKCRPDGFSNMTSSKAPCRKHTNCSYFGLLLPQKGNATHNIGCSNSEQ 401
 Db 141 VKCRPDGFSNMTSSKAPCRKHTNCSYFGLLLPQKGNATHNIGCSNSEQ 194
 RESULT 4
 ID 008727 PRELIMINARY; PRT; 401 AA.
 AC 008727;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF).
 GN TNFRSF11B OR OPG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE; 97262071.
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehry R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Day E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RA *Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density";
 RL Cell 89:309-319(1997).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC EMBL: U94330; AAB53707.1; -.
 CC HSSP: P25942; ICDF.
 CC INTERPRO: IPR001368; -.
 CC PIRAM: PF00020; TNFR_C6; 4.
 CC PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 CC PROSITE: PS50050; TNFR_NGFR_2; 2.
 CC KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT DOMAIN 23 201
 FT REPEAT 23 201
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT DOMAIN 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 165
 FT CARBOHYD 178 178
 FT CARBOHYD 178 289
 FT CARBOHYD 138 289
 FT VARIANT 138 289
 FT VARIANT 161 161
 FT VARIANT 165 165
 FT VARIANT 288 288
 FT VARIANT 296 296
 FT SEQUENCE 401 AA; 46192 MW; FDC6A31F1D4E573A CRC64;
 Query Match 39.0%; Score 875; DB 11; Length 401;
 Best Local Similarity 85.5%; Pred. No. 2.9e-68;
 Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

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QY 228 KETPPKYLHDETSKOLCDKCPGTYLKONHTAKMKYCAPCPDHYTDSMTSDEC 287
DB 21 QETPPKYLHDETSKOLCDKCPGTYLKONHTAKMKYCAPCPDHYTDSMTSDEC 80
QY 288 LYSPVCKELOYVQECNRTNHRVCECKEGRYLEIEFLCKHRSCPPGFGVVOAGTPEPNT 347
DB 81 VYSPVCKELOYVQECNRTNHRVCECKEGRYLEIEFLCKHRSCPPGFGVVOAGTPEPNT 140
QY 348 VCKRCPDGFSSNETSKAPCKRHTNCVSFGLLLTOKGNATIDNICSQNSESTQ 400
DB 141 VCKRCPDGFSSNETSKAPCKRHTNCVSFGLLLTOKGNATIDNICSQNSESTQ 193

RESULT 5
Q9RI4 PRELIMINARY; PRT; 437 AA.
AC Q9RI4;
RT 01-MAY-2000 (TEMBLrel. 13, Created)
RT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
RT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB (FRAGMENT).
OS Mus. musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramodoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: A6152372; AAD0243.1; -
DR INTERPRO: IPR000495; -
DR INTERPRO: IPR003066; -
DR PFAM: PF00047; 1g; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 437
FT NON_TER 1 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7B33E7D697C CRC64;

Query Match 36.7%; Score 824.5; DB 11; Length 437;
Best Local Similarity 62.9%; Pred. No. 8e-64;
Matches 141; Conservative 43; Mismatches 35; Indels 5; Gaps 2;

QY 7 CYP--CPAPELLGSPVFLPPPKDLMISRPDEVTGVVVDVSHEDPEVKNYVDGVE 64
DB 217 CKPCICVPEV---SVVFIPPKPKDVLITLTPKVCVVVDISKDDPEVQFSWFVDVE 273
QY 65 VHAATKPREDOVSTYRVVSVLVTLVHODWLNKGEYCKYSNKLAPRIETISKAGOP 124
DB 274 VHAATQTPREDOVSTYRVVSELPIHODWLNKGEYCKYSNKLAPRIETISKAGOP 333
QY 125 REPQVYTLPPSRDELTKNOVSLTLVGFPYSDIAVEMESGQENNYKTTTPYLDSDGS 184
DB 334 KAPQVYTLPPSRDEKMAKDKVSLTGMITDFPEDITVEMQWGAENYKNTQPIINDDGS 393
QY 185 FELYSKLTVDKSRWQGNVSCSYMHALNNHYTKSLISPGK 228
DB 394 YFYSKLNVOKSRWQGNVSCSYMHALNNHYTKSLISPGK 437

RESULT 6
Q95407 PRELIMINARY; PRT; 300 AA.
AC Q95407;
RT 01-MAY-1999 (TEMBLrel. 10, Created)
RT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
RT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE DECOY RECEPTOR 3.
DE DCR3 OR TR6.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99087326.
RA Pitt R.M., Masters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RT Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD.
RX MEDLINE: 99253915.
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RT J. Biol. Chem. 274:13733-13736(1999).
DR EMBL: AF104419; AAD03056.1; -
DR EMBL: AF134240; AAD29688.1; -
DR HSSP: P25942; ICDF.
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR001368; -
DR PFAM: PF000020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;

Query Match 19.3%; Score 433; DB 4; Length 300;
Best Local Similarity 42.9%; Pred. No. 5.4e-30;
Matches 69; Conservative 29; Mismatches 63; Indels 0; Gaps 0;

QY 233 KYLHDETSKOLCDKCPGTYLKONHTAKMKYCAPCPDHYTDSMTSDECYCS 292
DB 34 PTPYWRDAETGERLVCAQCPCPGTFVORPCRDSPPTCGPCPPHYTQFNMYLERCRYCN 93
QY 293 VCKELOYVQECNRTNHRVCECKEGRYLEIEFLCKHRSCPPGFGVVOAGTPEPNTVCKRC 352
DB 94 LCGREBEAACHATNHRACRCRTGFFAHAGFLEHASCPCGAGVIAPIPSQNTQCOPC 153
QY 353 PDGFFSNETSAPCKRHTNCVSFGLLLTOKGNATIDNICS 393
DB 154 PDGFFSNETSAPCKRHTNCVSFGLLLTOKGNATIDNICS 194

RESULT 7
Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
RT 01-MAY-2000 (TEMBLrel. 13, Created)
RT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
RT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE DECOY RECEPTOR.
OS Salvelinus fontinalis (Brook trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Plectanctopterygii; Salmoniformes; Salmonidae; Salvelinus.
RN [1]
RP SEQUENCE FROM N.A.
RA Bode J., Goetz F.W.;
RT "A tumor necrosis factor receptor homolog is up-regulated in the brook
RT trout (Salvelinus fontinalis) cvary at the completion of ovulation.";
RT Biol. Reprod. 0:0-0(1999).
DR EMBL: AF156738; AAD56428.1; -
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR001368; -
DR PFAM: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.

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"A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks."

RT Nature 374:168-173(1995).
EMBL: U18701; AAB8195.1; -
DR INTERPRO: IPR000495; -
DR INTERPRO: IPR003006; -
DR PFM: PFO0047; 19; 6.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Signal.
FT SIGNAL 1 18
FT CHAIN 19 684
SQ SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6DFD CRC64;

Query Match 12.18; Score 272.5; DB 13; Length 684;
Best Local Similarity 33.3%; Pred. No. 1.3e-15;
Matches 71; Conservative 35; Mismatches 98; Indels 9; Gaps 7;

QY 20 SVFLPPKPKDLMISRPVTVVDSHEDPE-VKFNWVVDGVEVHNAKTRREGYN 78
459 SVSLKPK-PFEIWTQQTATVCEIV--YSDLENIKVFWOVNGVERKKVETONPEWSG 514

QY 79 STYRVSVLTLYHODWLNKGEYKCKVSNKALPAPIEKTISKAK-GOPREPQVYTLPPSRD 137
515 SKSTIVSKLKMASEMSPGCTEYVCLVEDSELPTPKASIRKANSQMHPRVYLHPSTD 574

QY 138 EL-TKNQVSLTCLVKGYPSPDIAMWESNGO-PENNYKTPPVLDSDGSEFLYKLYDK 195
575 EIDENSATLMLCLATNHPAIEYVGMANDRLDLSGRYTVQDSEKSSSVTRDLRLTA 634

QY 196 SRMQGVNFSVGMHNLHNYTOKSLSPCK 228
DB 635 AEMNSDTTYSCLVGHPSL-NRDLIRSTKSNKG 666

RESULT 14
QY606 PRELIMINARY; PRT; 616 AA.

AC QY606;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF11A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
[1]
SEQUENCE FROM N.A.
RX MEDLINE: 98032977.
RA Anderson D.W., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Gilbert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
RL Nature 390:175-179(1997).
CC - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC - TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL GLAND.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: AF018253; AAB86809.1; -
DR MIM: 603499; -
DR INTERPRO: IPR001368; -
DR PFM: PFO0020; TNFR_c6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT SIGNAL 1 22
FT CHAIN 23 616
FT DOMAIN 24 212
EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 213 233
FT DOMAIN 234 616
FT SIGNAL 235 616
FT CHAIN 236 616
FT REPEAT 33 195
FT REPEAT 33 195
FT REPEAT 70 112
FT REPEAT 113 152
FT REPEAT 153 195
FT DISULFID 34 46
FT DISULFID 47 60
FT DISULFID 50 68
FT DISULFID 71 86
FT DISULFID 92 112
FT DISULFID 114 124
FT DISULFID 126 133
FT DISULFID 127 131
FT DISULFID 154 169
FT DISULFID 175 194
FT CARBOHYD 105 105
FT CARBOHYD 174 174
SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;

Query Match 11.2%; Score 252.5; DB 4; Length 616;
Best Local Similarity 36.6%; Pred. No. 6.3e-14;
Matches 56; Conservative 17; Mismatches 73; Indels 7; Gaps 4;

QY 248 CDKCPSTYKQKQHTAKVTCAPCPDHYTDSMHSDECLYSPVC--KEIQYKQEC 304
47 CNKPEPKYMSKCTTSDSCVLCPCGDEYLDISNEEDKCL-LHKVCDTGKALAAVAVAG- 104

QY 305 NRTINRCECKEGRY--LEIEFLKHKSCPPGFGVQAGPRTVTKRRPDGFSNETS 362
105 NSTTPRCACGTAGYHMSQDCECCRNTECAPGLAQHPQLQNDYVCKPCLAGYFSDAFS 164

QY 363 SKAPCRKNTCSVGLLITQGNATHDNICGN 395
DB 165 STDKCRPWTNCTFLGKRVHGHTEKSDAVCSS 197

RESULT 15
O35305 PRELIMINARY; PRT; 625 AA.

AC O35305;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF11A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
RX MEDLINE: 98032977.
RA Anderson D.W., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Gilbert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
RL Nature 390:175-179(1997).
CC - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: AF019046; AAB86810.1; -
DR HSSP: P25942; 1CDF.
DR MGD: MGI:1314891; Tnfstfla.
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR001368; -
DR PFM: PFO0020; TNFR_c6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.

DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 KM Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 625 RECEPTOR ACTIVATOR OF NF-KAPPA-B.
 FT DOMAIN 31 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 235 POTENTIAL.
 FT DOMAIN 236 625 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 196 4 X TNFR-CYS.
 FT REPEAT 34 70 TNFR-CYS 1.
 FT REPEAT 71 114 TNFR-CYS 2.
 FT REPEAT 115 153 TNFR-CYS 3.
 FT REPEAT 154 196 TNFR-CYS 4.
 FT DISULFID 35 47 BY SIMILARITY.
 FT DISULFID 48 61 BY SIMILARITY.
 FT DISULFID 51 69 BY SIMILARITY.
 FT DISULFID 72 87 BY SIMILARITY.
 FT DISULFID 93 113 BY SIMILARITY.
 FT DISULFID 115 125 BY SIMILARITY.
 FT DISULFID 127 134 BY SIMILARITY.
 FT DISULFID 128 152 BY SIMILARITY.
 FT DISULFID 155 170 BY SIMILARITY.
 FT DISULFID 176 195 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;

Query Match 11.2%; Score 252.5; DB 11; Length 625;
 Best Local Similarity 36.6%; Pred. No. 6.4e-14;
 Matches 56; Conservative 18; Mismatches 72; Indels 7; Gaps 4;

OY 248 CDKCPGTYLKGHCIAKMTVCAPCPDHYYTDSWHTSDECIYCSPVC--KEIQYVKQEC 304
 DB 48 CSRCEPGKTLSSKCTPTSDSVCLPCGPEYLDPTWNEDEKCL-LHKVCDAGKALVAV-DPG 105
 OY 305 NRTNNVCECKEGRY--LEIEFCLKHRSCPGFGVVOAGTPERTVCKRCRCPDGFSENETS 362
 DB 106 NHTADRRCACTAGHYMNSDCCECCRRTECAFGAGHPQLINKDITVCTPCLLGFPSDVFS 165
 OY 363 SKAPCRKHTNCVFGILLTQKGNATHDNICSGN 395
 DB 166 STDCKPMTNCTILGKLEAHOGTSESDVVCSS 198

Search completed: December 27, 2000, 10:52:42
 Job time: 73 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:55:07 ; Search time 24.16 Seconds
(without alignments)
530.262 Million cell updates/sec

Title: US-09-389-545-8

Sequence: 1 MDKHTCPCCAPPELLGSPS.....QKGNATHDNICSGNSESTOK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Minimum number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1233 | 54.9 | 330 | 1 | GCL_HUMAN |
| 2 | 1142.5 | 50.9 | 336 | 1 | GCL_HUMAN |
| 3 | 1135 | 50.5 | 337 | 1 | GCL_HUMAN |
| 4 | 1126 | 50.1 | 280 | 1 | GCL_HUMAN |
| 5 | 918.5 | 40.9 | 333 | 1 | GC_RABIT |
| 6 | 889 | 39.6 | 329 | 1 | GC2_CAVO |
| 7 | 845.5 | 37.6 | 339 | 1 | GC3_MOUSE |
| 8 | 838 | 37.3 | 333 | 1 | GC3_MOUSE |
| 9 | 835.5 | 37.2 | 338 | 1 | GC3_MOUSE |
| 10 | 818.5 | 36.4 | 326 | 1 | GCL_RAT |
| 11 | 817.5 | 36.4 | 324 | 1 | GCL_MOUSE |
| 12 | 812.5 | 36.2 | 333 | 1 | GCL_MOUSE |
| 13 | 809.5 | 36.0 | 329 | 1 | GC2_MOUSE |
| 14 | 809 | 36.0 | 330 | 1 | GCA_MOUSE |
| 15 | 804 | 35.8 | 339 | 1 | GCA_MOUSE |
| 16 | 802 | 35.7 | 335 | 1 | GCA_MOUSE |
| 17 | 785.5 | 35.0 | 332 | 1 | GCA_MOUSE |
| 18 | 779 | 34.7 | 336 | 1 | GCB_MOUSE |
| 19 | 774 | 34.5 | 405 | 1 | GCB_MOUSE |
| 20 | 762 | 34.1 | 454 | 1 | GCB_MOUSE |
| 21 | 761 | 34.1 | 455 | 1 | GCB_MOUSE |
| 22 | 760 | 34.1 | 455 | 1 | GCB_MOUSE |
| 23 | 759 | 34.1 | 455 | 1 | GCB_MOUSE |
| 24 | 758 | 34.1 | 455 | 1 | GCB_MOUSE |
| 25 | 757 | 34.1 | 455 | 1 | GCB_MOUSE |
| 26 | 756 | 34.1 | 455 | 1 | GCB_MOUSE |
| 27 | 755 | 34.1 | 455 | 1 | GCB_MOUSE |
| 28 | 754 | 34.1 | 455 | 1 | GCB_MOUSE |
| 29 | 753 | 34.1 | 455 | 1 | GCB_MOUSE |
| 30 | 752 | 34.1 | 455 | 1 | GCB_MOUSE |
| 31 | 751 | 34.1 | 455 | 1 | GCB_MOUSE |
| 32 | 750 | 34.1 | 455 | 1 | GCB_MOUSE |
| 33 | 749 | 34.1 | 455 | 1 | GCB_MOUSE |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 303 | 13.5 | 438 | 1 | HVC2_HETFR | P23085 heterodontu |
| 35 | 299.5 | 13.3 | 299 | 1 | ALC_RABIT | P01879 oryctolagus |
| 36 | 293.5 | 13.1 | 438 | 1 | HVC2_HETFR | P23087 heterodontu |
| 37 | 287.5 | 12.8 | 446 | 1 | MOU_MOUSE | P01875 gallus gall |
| 38 | 284 | 12.6 | 289 | 1 | CD40_MOUSE | P27512 mus musculu |
| 39 | 282.5 | 12.6 | 393 | 1 | HVC3_HETFR | P23086 heterodontu |
| 40 | 278.5 | 12.4 | 461 | 1 | HVC4_HETFR | P23088 heterodontu |
| 41 | 278 | 12.4 | 461 | 1 | HVC1_HETFR | P23084 heterodontu |
| 42 | 276 | 12.3 | 353 | 1 | ALC1_HUMAN | P01876 homo sapien |
| 43 | 271.5 | 12.1 | 353 | 1 | ALC1_GORGO | P20758 gorilla gor |
| 44 | 271 | 12.1 | 340 | 1 | ALC1_HUMAN | P01877 homo sapien |
| 45 | 264 | 11.8 | 277 | 1 | CD40_HUMAN | P25942 homo sapien |

ALIGNMENTS

| RESULT | 1 | STANDARD | PRT | 330 AA. |
|--------|--|----------|-----|---------|
| AC | GCL_HUMAN | | | |
| AC | P01857 | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | |
| DE | IG GAMMA-1 CHAIN C REGION. | | | |
| GN | IGHG1. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE: 82274238. | | | |
| RA | Ellison J.W., Berson B.J., Hood L.E.; | | | |
| RT | "The nucleotide sequence of a human immunoglobulin C gamma1 gene."; | | | |
| RL | Nucleic Acids Res. 10:4071-4079(1982). | | | |
| RN | [2] | | | |
| RP | SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). | | | |
| RX | MEDLINE: 71064024. | | | |
| RA | Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.; | | | |
| RT | Waxdal M.J., Edelman G.M.; | | | |
| RL | "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; | | | |
| RN | Biochemistry 9:3161-3170(1970). | | | |
| RP | [3] | | | |
| RX | SEQUENCE OF 136-329 (EU). | | | |
| RA | Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.; | | | |
| RT | Edelman G.M.; | | | |
| RL | "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; | | | |
| RN | Biochemistry 9:3171-3181(1975). | | | |
| RP | [4] | | | |
| RX | SEQUENCE (MYELOMA PROTEIN N.E). | | | |
| RA | Medline: 77070269. | | | |
| RT | Bonstingl H., Hilschmann N.; | | | |
| RL | "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; | | | |
| RN | Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976). | | | |
| RP | [5] | | | |
| RX | SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. | | | |
| RA | Medline: 83289131. | | | |
| RT | Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; | | | |
| RL | "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; | | | |
| RN | Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983). | | | |
| RP | [6] | | | |
| RX | DISULFIDE BONDS. | | | |
| RA | Medline: 71064027. | | | |
| RT | Gall W.E., Edelman G.M.; | | | |
| RL | "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."; | | | |

Biochemistry 9:3188-3196(1970).

[17] DISULFIDE BONDS.

RA Dieker L., Schwarz J., Relchel W., Hilschmann N.;
 "Rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein NIE), I: Purification and
 characterization of the protein, the L- and H-chains, the
 cyanogen bromide cleavage products, and the disulfide bridges.";
 Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

RL [18] X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).

RA Delsenhofer J.;
 "Crystallographic refinement and atomic models of a human Fc fragment
 and its complex with fragment B of protein A from *Staphylococcus*
 aureus at 2.9- and 2.8-A resolution.";
 Biochemistry 20:2361-2370(1981).

CC [19] MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 MARKER & THE GIM (NON-1) MARKERS.

CC [20] MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 35,116,198,269 & 272.

CC [21] MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 268-272.

CC [22] MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 RESIDUES 198,267&272.

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 or send an email to license@sib-sib.ch).

CC [24] EMBL: J00228; AAC82527.1; ALT_INIT.

DR PIR: A02146; GHHT.

DR PDB: 1FC1; 15-JUL-92.

DR PDB: 1FC2; 15-JUL-92.

DR MIM: 147100; -

DR INTERPRO: IPR000495; -

DR INTERPRO: IPR003006; -

DR PFM: PF00047; 1g; 3.

DR PROSITE: PS00290; 1G_MHC; 2.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 3D-structure.

NON_TER 1 1

DOMAIN 99 98 CH1.

DOMAIN 111 110 HINGE.

DOMAIN 224 223 CH2.

DOMAIN 224 330 CH3.

DISULFID 27 83

DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).

DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).

DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).

DISULFID 144 204

DISULFID 250 308

CARBOHYD 180 97

VARIANT 97 97

VARIANT 239 239

VARIANT 241 241

VARIANT 241 241

MOD_RES 330 330

STRAND 123 126

HELIX 130 134

TURN 136 137

STRAND 141 148

STRAND 158 162

TURN 163 164

REMOVED POST-TRANSLATIONALLY.

FT STRAND 165 166

FT STRAND 175 178

FT STRAND 183 190

FT HELIX 193 197

FT TURN 198 199

FT STRAND 202 206

FT STRAND 215 219

FT STRAND 227 227

FT STRAND 230 234

FT HELIX 238 240

FT TURN 241 242

FT STRAND 245 256

FT STRAND 260 266

FT TURN 267 268

FT STRAND 274 276

FT STRAND 280 281

FT TURN 283 284

FT STRAND 287 296

FT HELIX 297 301

FT TURN 302 303

FT STRAND 306 312

FT TURN 313 314

FT TURN 316 317

FT STRAND 320 324

SEQUENCE 330 AA; 36106 MM; 3770E106C2FA33D CRC64;

Query Match 54.9%; Score 1233; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 8,9e-79;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKTHCPCPAPELIGGSVFLFPKPKDTLMISRTPEVTCVYVDVSHEDPEVKFNMTYVD 61
 DB 104 DKTHCPCPAPELIGGSVFLFPKPKDTLMISRTPEVTCVYVDVSHEDPEVKFNMTYVD 163

QY 62 GVEVNAKTKPREQYNSTYRVSVYLVHODMNGKCKVSKNALPAPLERTISAK 121
 DB 164 GVEVNAKTKPREQYNSTYRVSVYLVHODMNGKCKVSKNALPAPLERTISAK 223

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 181
 DB 224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 283

QY 182 DGSFELYSLTVDSKRWQGVFSCVYHEALHNHYTQKSLSLSPGK 228
 DB 284 DGSFELYSLTVDSKRWQGVFSCVYHEALHNHYTQKSLSLSPGK 330

RESULT 2

GC2_HUMAN STANDARD: PRT; 326 AA.

ID GC2_HUMAN

AC P01859;

DC 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

GN IG GAMMA-2 CHAIN C REGION.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 82197621.

RA Ellison J.W., Hood L.E.;
 "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes.";
 Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).

RN [2]

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).

RX MEDLINE; 81007873.

RA Wang A.-C., Tung E., Fudenberg H.H.;
 "The primary structure of a human IgG2 heavy chain: genetic,

RT evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [3]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE; 80001357.
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [4]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE; 80114419.
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [5]
 RP REVISIONS TO 25; 59: 60 AND 264-268 (ZIE).
 RX Hofmann T., Parr D.M.;
 RT Submitted (MAR-1980) to the PIR data bank.
 RN [6]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE; 95255298.
 RA Scoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE; 72033500.
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [8]
 RP DISULFIDE BONDS.
 RX MEDLINE; 69064124.
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: V00554; CAA23814.1; -;
 CC EMBL: V00554; CAA23815.1; -;
 CC EMBL: V00554; CAA23816.1; -;
 CC EMBL: V00554; CAA23817.1; -;
 CC PIR: A02148; G2HU.
 CC MIM: 147110; -;
 CC INTERPRO: IPR000495; -;
 CC INTERPRO: IPR003006; -;
 CC PRAM: PF00047; 19; 3.
 CC PROSITE: PS00290; IG_MHC; 2.
 CC Immunoglobulin domain; Immunoglobulin C region.
 CC KW IMMUNOGLOBULIN C region.
 CC FT NON_TER 1 98
 CC FT DOMAIN 1 98
 CC FT DOMAIN 99 110
 CC FT DOMAIN 111 219
 CC FT DOMAIN 220 326
 CC FT DISULFID 14 14
 CC FT DISULFID 27 83
 CC FT DISULFID 102 102
 CC FT DISULFID 103 103
 CC FT DISULFID 106 106
 CC FT DISULFID 109 109
 CC FT DISULFID 140 200
 CC FT DISULFID 246 304
 CC FT VARIANT 60 60
 CC S -> A (IN MYELOMA PROTEINS TIL & ZIE).

FT SITE 156 156 /FTID-VAR 003889.
 FT MOD_RES 326 326 AT OR NEAR THE COMPLEMENT-BINDING SITE.
 SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CE9C CRC64;
 Query Match 50.9%; Score 1142.5; DB 1; Length 326;
 Best Local Similarity 94.1%; Pred. No. 1,6e-72;
 Matches 209; Conservative 8; Mismatches 4; Indels 1; Gaps 1;
 Db 7 CPPEAPELLGSPVFLPPPKPKDTLMISRPETCVVNVSHEDPEVKRMVYDGEVH 66
 106 CPPEAPPP-VAGSVFLPPPKPKDTLMISRPETCVVNVSHEDPEVKRMVYDGEVH 164
 QY 67 NAKTKPREQYNSTRVSVLYVLAHODMLNGEKYCKVSKALPAPIEKTISKARQPRE 126
 165 NAKTKPREQDNSTRFRVSVLYVLAHODMLNGEKYCKVSKALPAPIEKTISKARQPRE 224
 Db 127 PQVTLPPSRDELTKNOVSLTCLVKGFPDIAVEMSNQPENNYTTTPVLDSDGSFF 186
 225 PQVTLPPSRDEMTKNOVSLTCLVKGFPDIAVEMSNQPENNYTTTPVLDSDGSFF 284
 QY 187 LYSKLTVDKSRMOQGNFSCSVMEALHNHYTKSLSPGK 228
 285 LYSKLTVDKSRMOQGNFSCSVMEALHNHYTKSLSPGK 326
 RESULT 3
 GC4_HUMAN STANDARD; PRT; 327 AA.
 ID GC4_HUMAN
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-4 CHAIN C REGION.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83157104.
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE; 70207560.
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RT constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: K01316; AAB59394.1; ALT_INIT.
 CC PIR: A02150; G4HU.
 CC MIM: 147130; -;
 CC INTERPRO: IPR000495; -;
 CC INTERPRO: IPR003006; -;
 CC PRAM: PF00047; 19; 3.
 CC PROSITE: PS00290; IG_MHC; 2.
 CC Immunoglobulin domain; Immunoglobulin C region.
 CC KW IMMUNOGLOBULIN C region.
 CC FT NON_TER 1 98
 CC FT DOMAIN 1 98
 CC FT DOMAIN 99 110
 CC FT DOMAIN 111 220
 CC FT HINGE 111 220
 CC FT HINGE 111 220

Best Local Similarity 90.3%; Pred. No. 2e-71; Matches 205; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKHTCPPEPAPPELLGGPSVFLFPPPKRDTLMISRTPEVTCVVDVSHEDPEVKFNMVVD 61
 DB 64 DTPPCPCRPAPPELLGGPSVFLFPPPKRDTLMISRTPEVTCVVDVSHEDPEVGFKNVVD 123
 QY 62 GVEHNNAKTRPREQYNTYRVSVLVTLVHODMNGEKYKKVSNKALPAIETIKSAK 121
 DB 124 GVOYHNNAKTRPREQYNTYRVSVLVTLVHODMNGEKYKKVSNKALPAIETIKSAK 183
 QY 122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 181
 DB 184 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 243
 QY 182 DGSFELYSKLTVDKSRMNOGQNVFSCSVMEALHNHYTOKSLSPGK 228
 DB 244 DGSFELYSKLTVDKSRMNOGQNVFSCSVMEALHNHYTOKSLSPGK 290

BULT 5
 ID GC_RABBIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA CHAIN C REGION.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 84030930.
 RX Bernstein K.E., Alexander C.B., Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 RT F-1 haplotype.";
 RL Immunogenetics 18:387-397(1983).
 RN [2]
 RP SEQUENCE OF 1-128.
 RX MEDLINE; 76135469.
 RA Pratt D.M., Mole L.E.;
 RT "Sequence studies on the constant region of the Fd sections of rabbit
 RT immunoglobulin G of different allotype.";
 RL Biochem. J. 151:337-349(1975).
 RN [2]
 RP SEQUENCE OF 88-266 FROM N.A.
 RA MEDLINE; 83299917.
 RX Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma
 RT heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 RT immunoglobulin G.";
 RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
 RT (in) Killander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 RL Stockholm (1967).
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER.
 CC 104-THR. AND THE E14 MARKER. 185-THR. REF.3 HAS THE D11 AND E15
 CC MARKERS AND REF.5 THE E15 MARKER.
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DR EMBL; M16426; AAA31289.1; -
 DR PIR; A02161; GHRB.
 DR INTERPRO; IPR000495; -
 DR INTERPRO; IPR003006; -
 DR PRAM; PF00047; 19; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER 1 104 104
 FT VARIANT 185 185
 FT CONFLICT 48 48
 FT CONFLICT 71 71
 FT CONFLICT 144 144
 FT CONFLICT 173 173
 FT CONFLICT 187 187
 FT CONFLICT 201 201
 FT CONFLICT 218 218
 FT CONFLICT 233 233
 FT CONFLICT 246 246
 FT CONFLICT 256 256
 FT CONFLICT 260 260
 FT CONFLICT 266 266
 FT CONFLICT 280 280
 FT CONFLICT 284 284
 SQ SEQUENCE 323 AA; 35404 MW; 69E8AA11B0579A8B CRC64;

Query Match 40.9%; Score 918.5; DB 1; Length 323;
 Best Local Similarity 71.7%; Pred. No. 5.4e-57;
 Matches 167; Conservative 29; Mismatches 32; Indels 5; Gaps 2;

QY 1 MDRK---HTC--PPCPPELLGGPSVFLFPPPKRDTLMISRTPEVTCVVDVSHEDPEVK*55
 DB 91 VDKTVAPSTCSKPTCPPELLGGPSVFLFPPPKRDTLMISRTPEVTCVVDVSHEDPEVQ 150
 QY 56 FNNYDGVENVNAKTRPREQYNTYRVSVLVTLVHODMNGEKYKKVSNKALPAIETIK 115
 DB 151 FTWYINNEQVTRAPPLREGQFNSTIRVSLTPITHODMNGEKYKKVSNKALPAIETIK 210
 QY 116 TISKAKGQPREQYNTYRVSVLVTLVHODMNGEKYKKVSNKALPAIETIK 175
 DB 211 TISKAKGQPREQYNTYRVSVLVTLVHODMNGEKYKKVSNKALPAIETIK 270
 QY 176 PNYDSDGSFELYSKLTVDKSRMNOGQNVFSCSVMEALHNHYTOKSLSPGK 228
 DB 271 PNYDSDGSFELYSKLTVDKSRMNOGQNVFSCSVMEALHNHYTOKSLSPGK 323

RESULT 6
 ID GC2_CAVPO STANDARD; PRT; 329 AA.
 AC P01862;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2 CHAIN C REGION.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 RN [1]
 RP SEQUENCE OF 1-3.
 RA Trischmann T.M.;
 RL Submitted (APR-1975) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 4-68.
 RX MEDLINE; 71058471.
 RA Birstein B.K., Hussain Q.Z., Gebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin G(2). 3. Amino acid sequence of the region around the

```

RT half-cystine joining heavy and light chains."
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE: 71058486.
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
  immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
  and hinge region cyanogen bromide fragments."
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE: 75036072.
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
  antibodies."
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE: 75036073.
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
  antibodies."
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE: 71058474.
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin."
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
  13 INBRED GUINEA PIGS.
DR PIR: A02151; G2GP.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 3.
DR PROSITE: PS00290; 1G_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
FT SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 39.6%; Score 889; DB 1; Length 329;
Best Local Similarity 72.3%; Pred. No. 6, 1e-55;
Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

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ID GC3 MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85027161.
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene."
RL EMBO J. 3:2041-2046(1984).
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CC -----
DR EMBL: J00451; -; NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 3.
DR PROSITE: PS00290; 1G_MHC; 1.
KW Immunoglobulin C region; Glycoprotein; Transmembrane;
KW Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT SEQUENCE 329 AA; 36228 MW; F45827174102BAD6 CRC64;

Query Match 37.6%; Score 845.5; DB 1; Length 329;
Best Local Similarity 67.0%; Pred. No. 6, 3e-52;
Matches 150; Conservative 34; Mismatches 37; Indels 3; Gaps 1;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89232738.
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0018; PS0018.
DR INTERPRO: IPR000495; -.
DR PIR: A02155; G3MSM.
DR INTERPRO: IPR003006; -.
DR PIR: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFD 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFD 27 80
FT DISULFD 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFD 147 207
FT DISULFD 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48DA60A6 CRC64;

Query Match 37.3%; Score 838; DB 1; Length 333;
Best Local Similarity 66.4%; Pred. No. 2,1e-51;
Matches 148; Conservative 33; Mismatches 42; Indels 0; Gaps 0;

OY 6 TCPPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHDEPFNMVYDGEV 65
DB 111 TCHKRPVELLGGPSVFIFPPKPKDILLISQNAKTCVVDVSEEPDQVGFYANNVY 170
OY 66 HNAKTRPEEOYNSTYRVSVLVTLVHODWLNGEKYCKVSNKALPAPIERTISAKGQPR 125
DB 171 HTAQOTPEEOYNSTYRVSVLVTLVHODWMSKEFKCKVNNKALPSPIERTISKRGIVR 230
OY 126 EQOYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPNNTKTPPVLDSDGSF 185
DB 231 KPOYVVMGPTEQLTEQVYSLTCLTSGFLPNDIGVMTSNGHIEKNKTEPVMDSDGSF 290
OY 186 FLYSKLTVDKSRMOQGNVFCSVMEHALNHNHTOKSLSLSPGK 228
DB 291 FMYSKLTNVRSRMDSRAPVVCVHVEGLNHNHVEKSLSPGK 333

RESULT 9
GC3M_MOUSE STANDARD: PRT: 398 AA.
ID GC3M_MOUSE P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85027161.
RA Weis J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE: 84041483.
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00451; AAB59655.1; -.
DR EMBL: V01526; CAA24767.1; ALT_SEQ.
DR PIR: A02155; G3MSM.
DR INTERPRO: IPR000495; -.
DR PIR: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein;
FT NON_TER 1
FT DISULFD 1 1
FT DOMAIN 98 113 CH1.
FT DOMAIN 114 223 HINGE.
FT DOMAIN 224 327 CH2.
FT TRANSMEM 346 362 CH3.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333
FT CONFLICT 342 342 E -> G (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 37.2%; Score 835.5; DB 1; Length 398;
Best Local Similarity 66.2%; Pred. No. 3,9e-51;
Matches 149; Conservative 34; Mismatches 39; Indels 3; Gaps 1;

OY 8 PP--CPAPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHDEPFNMVYDGEV 64
DB 106 PPGSSCPGNILGSPSVIFPPKPKDALMISLTPVTCVVDVSDDDVHSMFVDNKE 165
OY 65 VNAKTRPEEOYNSTYRVSVLVTLVHODWLNGEKYCKVSNKALPAPIERTISAKGQPR 124
DB 166 VHTAQOTPEEOYNSTYRVSVLVTLVHODWMSKEFKCKVNNKALPAPIERTISKRGIVR 225
OY 125 REPOYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPNNTKTPPVLDSDGS 184
DB 226 QTPQYVTLPPSRDELTKNOVSLTCLVTFSEALISVEMERNGELEDQTKNTPPIIDSDGT 285
OY 185 FLYSKLTVDKSRMOQGNVFCSVMEHALNHNHTOKSLSLSPGK 229
DB 286 YFLYSKLTVDSDMSWLGELIFTCVHVEALNHNHHTOKSLSPGK 330

RESULT 10
GC1_RAT STANDARD: PRT: 326 AA.
ID GC1_RAT P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89232738.
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0017; PS0017.
DR INTERPRO: IPR000495; -.
DR PIR: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein.

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FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB5EF49B5DA CRC64; N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 36.4%; Score 818.5; DB 1; Length 326;
Best Local Similarity 63.1%; Pred. No. 4.7e-50;
Matches 142; Conservative 41; Mismatches 35; Indels 7; Gaps 2;

7 CPGCPABELLG---PSVLFPPKPKDITLMISRTPEVTCVYVDSHEDPEVKNWYDGV 63
106 CKPC---ICTGEVSVFIFPPKPKDVLITLTPKVTQVVDISODPEVHFSWFDV 161
64 EVHNAKTPREEDQNSTYRYVSVLTVLHODMLNGKEKCVSKALPAPLEKTSKAGQ 123
162 EVHTAOTRPEEDQNSTFRSVSELPIMHODMLNGKTRCKVTSNAAPSPLEKTSKPEGR 221
124 PREPOVYTLPPSDELTKNQVSLTCLVKGFPSPDIAVWESNGOPENNYKTPPVLDSDG 183
222 TVPHTVYTPMPTKEEMTQNEVSTICWKGFYPIVYEWQMGQPAENYKNTPTMDTDG 281
QY 184 SFLLYSKLTVDKSRMOQGNFSCSVYHAEALHNHYTKSLSTSGK 228
DB 282 SYFLSKLVNOKSKNWEAGNTFTCSVLHGLHNHRTKSLSHSPGK 326

RESULT 11
GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
OS Mus musculus (Mouse).
NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
NP SEQUENCE FROM N.A.
RX MEDLINE: 80045036.
RA Honjo T., Obara M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene."
RT Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE: 80202559.
RA Obara M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT cloned in a bacterial plasmid."
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE: 80012837.
RA Rogers J., Clarke P., Salsner M.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT heavy chain."
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).

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RX MEDLINE: 78242288.
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
RT murine myeloma gamma1 chain."
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE: 73008889.
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein."
RL Biochem. J. 126:837-850(1972).
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DR EMBL: V00793; CAA24172.1; -
DR EMBL: V00793; CAA24173.1; -
DR EMBL: V00793; CAA24174.1; -
DR EMBL: V00793; CAA24175.1; -
DR EMBL: V00795; CAA24176.1; -
DR PIR: A02159; GIMS.
DR MGD: MGI:96446; IGH-4.
DR INTERPRO: IPR000495; -
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; Ig; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 174 374 N-LINKED (GLCNAC. .).
FT CARBOHYD 174 374
FT DISULFID 244 302
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 36.4%; Score 817.5; DB 1; Length 324;
Best Local Similarity 62.5%; Pred. No. 5.4e-50;
Matches 140; Conservative 44; Mismatches 35; Indels 5; Gaps 2;

7 CPGCPABELLGSPSVLFPPKPKDITLMISRTPEVTCVYVDSHEDPEVKNWYDGV 64
104 CKPCICTPEV---SSVLFPPKPKDVLITLTPKVTQVVDISODPEVQFSWFDVDE 160
QY 65 VHAHNAKTPREEDQNSTYRYVSVLTVLHODMLNGKEKCVSKALPAPLEKTSKAGCP 124
DB 161 VHTAOTRPEEDQNSTFRSVSELPIMHODMLNGKTRCKVTSNAAPSPLEKTSKPEGR 220
QY 125 REPQVYTLPPSDELTKNQVSLTCLVKGFPSPDIAVWESNGOPENNYKTPPVLDSDGS 184
DB 221 KAPOVYTLPPPEQNAKDKVSLTCLMITEFPEPDIYVWQMGQPAENYKNTQPIINWTS 280
QY 185 SFLLYSKLTVDKSRMOQGNFSCSVYHAEALHNHYTKSLSTSGK 228
DB 281 YFYSKLVNOKSKNWEAGNTFTCSVLHGLHNHRTKSLSHSPGK 324

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RESULT 12
 GCIM_MOUSE STANDARD: PRT: 393 AA.
 ID GCIM_MOUSE
 AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 80045036.
 RA Honjo T., Odate M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene.";
 RT Cell 18:559-568(1979).
 [2]
 SEQUENCE OF 323-393 FROM N.A.
 MEDLINE: 82197626.
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly
 conserved transmembrane sequence and a 28-residue intracellular
 domain.";
 RT Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 [3]
 SEQUENCE OF 323-366 FROM N.A.
 MEDLINE: 82115295.
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl terminal of
 immunoglobulin gamma chains.";
 RT Cell 26:19-27(1981).
 [4]
 SEQUENCE OF 1-44 FROM N.A.
 MEDLINE: 82222190.
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 immunoglobulin gamma chains.";
 RT Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO mRNA
 SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
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 or send an email to license@isb-sib.ch).
 CC EMBL: V00793; CAA24172.1;
 CC EMBL: V00793; CAA24173.1;
 CC EMBL: V00793; CAA24174.1;
 DR PIR: B02159; GIMSM.
 DR MGD: MGI:96446; IGH-4.
 DR INTERPRO: IPR000495;
 DR INTERPRO: IPR003006;
 DR PFM: PFO0047; 19; 3.
 DR PROSITE: PS00290; IGH_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 Alternative splicing; Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.

FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT DISULFID 244 302.
 FT TRANSMEM 340 357
 FT DOMAIN 358 393 POTENTIAL.
 FT SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64; CYTOPLASMIC (POTENTIAL).
 Query Match 36.2%; Score 812.5; DB 1; Length 393;
 Best Local Similarity 62.3%; Pred. No. 1.5e-49;
 Matches 139; Conservative 44; Mismatches 35; Indels 5; Gaps 2;
 QY 7 CPE--CPAPELGSPVVFEPPEPKDLMISRTPEYGVVDVSHDEPKFKNWYDGYE 64
 DB 104 CKPCICTVPEV---SSVFIPPEPKDYLITLTPKVTGVYDIDSKDPEVOFSWFVDYVE 160
 QY 65 VHNKTRPREOYNSTYRVSVTLVLDHDLNGEKYKRVNKLPAPIEKTISKAKGP 124
 DB 161 VHTAQTPREOYNSTYRVSVTLVLDHDLNGEKYKRVNKLPAPIEKTISKAKGP 220
 QY 125 REPQVTLPPSRDELTKNOVSLTCLVKGFPSPDIANVESNGOPENNYKTPPVLDSDG 184
 DB 221 KAPQVYTIPEPKDMARKDKVSLTCLMIDFEDITVENOMGPAENYKTPPVLDSDG 280
 QY 185 FFLYSKLTVDKSRMONGNFCVSMHEALHNHYTOKSLSLSPG 227
 DB 281 YFYISKLVNOKSMWENGTFTCSVLHDEGLHNHHTKSLSHSPG 323
 RESULT 13
 GCC_RAT
 ID GCC_RAT STANDARD: PRT: 329 AA.
 AC P20762;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2C CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86166903.
 RA Bruggemann M., Delmasstro-Galfré P., Waldmann H., Calabi F.;
 RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
 region cDNA: extensive homology to mouse gamma 3.";
 RT Eur. J. Immunol. 18:317-319(1988).
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 or send an email to license@isb-sib.ch).
 CC EMBL: X07189; CAA30169.1;
 DR PIR: S00847; S00847.
 DR INTERPRO: IPR000495;
 DR INTERPRO: IPR003006;
 DR PFM: PFO0047; 19; 3.
 DR PROSITE: PS00290; IGH_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 222 CH2.
 FT DOMAIN 223 329 CH3.

```

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCDD7B7933850773 CRC64;

Query Match 36.0%; Score 809.5; DB 1; Length 329;
Best Local Similarity 63.8%; Pred. No. 2e-49;
Matches 143; Conservative 41; Mismatches 37; Indels 3; Gaps 1;

OY 8 PP---CPAPELLGSPSVLEFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNMYDVGVE 64
DB PPTDCSDNDNGRPVSFLEFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNMYDVGVE 165
OY 65 VHNATKPREDOYNSTYRVSVLTVLHODWLNKREYCKVSNKALPAPIERTISKARQOP 124
166 VTAQTQPHEDQNGTFRVSVLTFLHODWLNKREYCKVSNKALPAPIERTISKARQOP 225
OY 125 REPQYITLPPSRDELTKNOVSLTCLVKGFPDIAVWESNGQPENNKTKTPPYLDSGDS 184
DB 226 RPPQYITLPPSRDESKKNVSLTCLVKGFPDIAVWESNGQPENNKTKTPPYLDSGDS 285
OY 185 FELYSKLTVDRKSRMOQGVFSCVYHNEALHNHYTKSLSPGK 228
DB 286 YFLYSKLVDRKSRMOQGVFSCVYHNEALHNHYTKSLSPGK 329

RESULT 14
GCAM_MOUSE STANDARD; PRT; 330 AA.
ID GCAM_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-2A CHAIN C REGION, A ALLELE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN (1)
RX MEDLINE: 81076554.
RA Sikorav J.-L., Aufray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA."
RL Nucleic Acids Res. 8:3143-3155(1980).
RN (2)
RX MEDLINE: 81198976.
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer."
RL Nucleic Acids Res. 9:1365-1381(1981).
RN (3)
RX MEDLINE: 81223894.
RA Olio R., Aufray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigene
RT family."
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN (4)
RX MEDLINE: 74175517.
RA Bourgeois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function."
RL Eur. J. Biochem. 43:423-435(1974).
RN (5)

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RP DISULFIDE BONDS.
RX MEDLINE: 73056887.
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges."
RL Eur. J. Biochem. 30:452-462(1972).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: V00798; CAA24178.1; -.
DR PIR: A02152; GZMSA.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFM: PFM00047; 1q; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KM Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64; REMOVED POST-TRANSLATIONALLY.

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Query Match 36.0%; Score 809; DB 1; Length 330;
Best Local Similarity 65.2%; Pred. No. 2.2e-49;
Matches 146; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

OY 7 CPP---CPAPELLGSPSVLEFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNMYDVGVE 64
DB 107 CPCKCPAPNLGSPSVLEFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNMYDVGVE 166
OY 65 VHNATKPREDOYNSTYRVSVLTVLHODWLNKREYCKVSNKALPAPIERTISKARQOP 124
DB 167 VHTAQTHREDYNSLTFLRVSVLPIQHDWLNKREYCKVSNKALPAPIERTISKARQOP 226
OY 125 REPQYITLPPSRDELTKNOVSLTCLVKGFPDIAVWESNGQPENNKTKTPPYLDSGDS 184
DB 227 RAPQYITLPPSRDEMTKNOVSLTCLVKGFPDIAVWESNGQPENNKTKTPPYLDSGDS 286
OY 185 FELYSKLTVDRKSRMOQGVFSCVYHNEALHNHYTKSLSPGK 228
DB 287 YFLYSKLVDRKSRMOQGVFSCVYHNEALHNHYTKSLSPGK 330

RESULT 15
GCAM_MOUSE STANDARD; PRT; 399 AA.
ID GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2A CHAIN C REGION, MEMBER-BOUND FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN (1)
RX MEDLINE: 82222190.
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

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CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
CC THE A ALLELE.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00471; AAB59661.1; ALT_INIT.
DR PIR: A02154; G2MSAM.
DR MGD: MG1:96443; IGH-1.
DR INTERPRO: IPR000495; -
DR INTERPRO: IPR003006; -
DR PRAM: PF00047; 19; 3.
DR PROSITE: PS00290; IGH_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363
FT DOMAIN 364 399
FT CARBOHYD 180 180
SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 35.88; Score 804; DB 1; Length 399;
Best Local Similarity 65.08; Pred. No. 5.9e-49;
Matches 145; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY 7 CYP--CPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVE 64
107 CPGCKCPAPNLGGPSVFLPPPKIKDVLIMISLPIVTCVVDVSEDDPDVQISMFNANVE 166
65 VHNAKTPREQVNSTYRVVSVLTVLHODVLNGEKYCKVSNKALPAPIEKTISKAKGP 124
167 VHTAQTGTHREDYNSLTRVVSALPIOHODWMSGKEFKCKVNNKDLPAPIERTISKPGSV 226
QY 125 REPOVYTLPPSRDELTKNOVSLTCLVGEVPSDIIVAVEMESNGOPENNYKTPPLDSDGS 184
227 RAPQVYVLPPEEEMTKQVTLTCVTDPMEDILYEPTNNGKTELNKNTPEVLDSDGS 286
Db 185 FFYLSKLTVDKSRWQGNVFSQVYHVALHNHYTKSLSPG-227
287 YFMYSKLRVEKKMVERNSYSCSVHGLNHNHTTKSFRTPG 329

Search completed: December 27, 2000, 10:55:08
Job time: 210 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2000, 10:54:39 ; Search time 40.66 Seconds

(without alignments)
625,862 Million cell updates/sec

Title: US-09-389-545-8

Sequence: 1 MDKHTCPCPAPPELLGSPS.....OKGNATHDNICSGNSESTOK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 65: *
1: pirl: *
2: pirl: *
3: pirl: *
4: pirl: *

Pred. No. is the number of results predicted to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|--------|---------------------|
| 1 | 1233 | 54.9 | 255 | 4 | S31866 | Ig gamma-1 chain |
| 2 | 1233 | 54.9 | 330 | 1 | GHHU | Ig gamma-1 chain |
| 3 | 1227 | 54.6 | 374 | 2 | S69339 | Ig heavy chain V |
| 4 | 1227 | 54.6 | 374 | 2 | S72664 | Ig heavy chain V |
| 5 | 1180 | 52.5 | 234 | 2 | PT0207 | Ig gamma chain C |
| 6 | 1146 | 51.0 | 377 | 2 | A23511 | Ig gamma-3 chain |
| 7 | 1144 | 50.9 | 377 | 2 | A60764 | Ig gamma-3 chain |
| 8 | 1142.5 | 50.9 | 326 | 1 | G2HU | Ig gamma-2 chain |
| 9 | 1135 | 50.5 | 327 | 1 | G4HU | Ig gamma-2 chain |
| 10 | 1121 | 49.9 | 289 | 1 | G3HUI | Ig gamma-4 chain |
| 11 | 918.5 | 40.9 | 333 | 1 | GHRB | Ig gamma-3 heavy |
| 12 | 906.5 | 40.4 | 328 | 2 | I47160 | Ig gamma chain C |
| 13 | 906.5 | 40.4 | 328 | 2 | I47159 | Ig gamma 2b chain |
| 14 | 903.5 | 40.2 | 277 | 2 | I47162 | Ig gamma 2a chain |
| 15 | 889 | 39.6 | 329 | 1 | G2GP | Ig gamma 4 chain |
| 16 | 885.5 | 39.4 | 328 | 2 | I47158 | Ig gamma-2 chain |
| 17 | 878.5 | 39.1 | 328 | 2 | I47161 | Ig gamma 1 chain |
| 18 | 855.5 | 38.1 | 470 | 2 | S22080 | Ig gamma 3 chain |
| 19 | 846 | 37.7 | 308 | 2 | C30554 | Ig heavy chain C |
| 20 | 846 | 37.7 | 472 | 2 | S31459 | Ig heavy chain C |
| 21 | 845.5 | 37.6 | 329 | 1 | G3MSC | Ig gamma-1 chain |
| 22 | 838 | 37.3 | 333 | 2 | PS0018 | Ig gamma-3 chain |
| 23 | 835.5 | 37.2 | 398 | 1 | G3MSM | Ig gamma-2b chain |
| 24 | 827.5 | 36.8 | 444 | 2 | PC4436 | Ig gamma-3 chain |
| 25 | 818.5 | 36.4 | 326 | 2 | PS0017 | monoclonal antibody |
| 26 | 817.5 | 36.4 | 324 | 1 | G1MS | Ig gamma-1 chain |
| 27 | 812.5 | 36.2 | 393 | 1 | G1MSM | Ig gamma-1 chain |
| 28 | 809.5 | 36.0 | 329 | 2 | S00847 | Ig gamma-2c chain |
| 29 | 809 | 36.0 | 330 | 1 | G2MSA | Ig gamma-2a chain |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 809 | 36.0 | 469 | 2 | S37483 | Ig gamma-2a chain |
| 31 | 804 | 35.8 | 399 | 1 | G2MSAM | Ig gamma-2a chain |
| 32 | 802 | 35.7 | 335 | 1 | G2MSAB | Ig gamma-2a chain |
| 33 | 794 | 35.0 | 446 | 2 | S40295 | Ig gamma-2a chain |
| 34 | 785.5 | 35.0 | 322 | 2 | PS0019 | Ig gamma-2a chain |
| 35 | 779 | 34.7 | 336 | 1 | G2MS11 | Ig gamma-2b chain |
| 36 | 779 | 34.7 | 474 | 2 | S25057 | Ig gamma-2b chain |
| 37 | 774 | 34.5 | 405 | 1 | G2MSBM | Ig gamma-2b chain |
| 38 | 764 | 34.0 | 327 | 2 | S06611 | Ig gamma-2 chain C |
| 39 | 757 | 33.7 | 475 | 2 | S01321 | Ig gamma-2b chain |
| 40 | 707 | 31.5 | 180 | 2 | I46732 | Ig gamma heavy cha |
| 41 | 577.5 | 25.7 | 249 | 2 | S69340 | Ig heavy chain VHI |
| 42 | 574.5 | 25.6 | 218 | 2 | A36040 | Ig heavy chain V-I |
| 43 | 571 | 25.4 | 152 | 2 | S14236 | Ig gamma-1 chain C |
| 44 | 395.5 | 17.6 | 572 | 2 | B46529 | Ig Y heavy chain (|
| 45 | 362 | 16.1 | 343 | 2 | S25644 | Ig mu chain C regi |

ALIGNMENTS

```
RESULT 1
S31866
Ig gamma-1 chain C region - synthetic
C/Species: synthetic
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C/Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C/Accession: S31866
R:Filipula, D.
Submitted to the EMBL Data Library, February 1993
A/Description: Screening method for protein-protein interactions of cloned gene produc
A/Reference number: S31866
A/Accession: S31866
A/Molecule type: mRNA
A/Residues: 1-255 <FIL>
A/Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C/Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match          54.9%  Score 1233; DB 4; Length 255;
Best Local Similarity 100.0%  Pred. No. 9.6e-72;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 DKHTCPCPAPPELLGSPVFLPPPKKDTLMSRPPEVTCVYVDVSHEDPEVKFNNYVD 61
    |||||
Db  29 DKHTCPCPAPPELLGSPVFLPPPKKDTLMSRPPEVTCVYVDVSHEDPEVKFNNYVD 88

QY  62 GVEYHNKTKPREQYNSITRVYSVLTVLHODMLNGKEYCKYSNKAAPAPIEKTISKAK 121
    |||||
Db  89 GVEYHNKTKPREQYNSITRVYSVLTVLHODMLNGKEYCKYSNKAAPAPIEKTISKAK 148

QY  122 GQPEPQVYTLPPSRDELTKNOVSLTCTVKGFPSPDLAVEMESGQPENNYKTTTPVLDS 181
    |||||
Db  149 GQPEPQVYTLPPSRDELTKNOVSLTCTVKGFPSPDLAVEMESGQPENNYKTTTPVLDS 208

QY  182 DGSEFLSKLTVDKSRWQGNV73CSVMHDLNHNHYOKSLSPGK 228
    |||||
Db  209 DGSEFLSKLTVDKSRWQGNV73CSVMHDLNHNHYOKSLSPGK 255

RESULT 2
GHHU
Ig gamma-1 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A/Reference number: A93433; MUID:82274238
A/Accession: A93433
```

A:Molecule type: DNA
 A:Residues: 1-330 <ELL>
 A:Cross-references: EMBL:Z17370
 A:Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers,
 A:Note: Lys-330 is removed after translation
 R:Harris, L.J.
 Submitted to the EMBL Data Library, October 1992
 A:Reference number: S33904
 A:Accession: S33861
 A:Molecule type: DNA
 A:Residues: 2-330 <HAR>
 A:Cross-references: EMBL:Z17370
 R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.
 Cell 29, 671-679, 1982
 A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
 A:Reference number: S33887; MUID:83001943
 A:Accession: S33887
 A:Molecule type: DNA
 A:Residues: 88-113:235-330 <TAK>
 A:Cross-references: EMBL:Z17370
 R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Maxdal, M.J.; Edelman,
 Biochemistry 9, 3161-3170, 1970
 A:Title: The covalent structure of a human gammag-immunoglobulin. VII. Amino acid sequen
 A:Reference number: A90563; MUID:71064024
 A:Contents: myeloma protein Eu
 A:Accession: B90563
 A:Molecule type: Protein
 A:Residues: 1-96, 'R', 98-135 <CON>
 A:Note: this sequence has the Gln(3) marker, 97-Arg
 R:Rutishauser, U.; Cunningham, B.A.; Bennett, G.; Konigsberg, W.H.; Edelman, G.M.
 Biochemistry 9, 3171-3181, 1970
 A:Title: The covalent structure of a human gammag-immunoglobulin. VIII. Amino acid sequen
 A:Reference number: A90564; MUID:71064025
 A:Contents: Eu
 A:Accession: A90564
 A:Molecule type: Protein
 A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
 A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
 R:Ponstingl, H.; Hilschmann, N.
 Hoppe-Sejler's Z. Physiol. Chem. 357, 1571-1604, 1976
 A:Title: Die Primerstruktur elnes monoklonalen IgG1-Immunglobulins (Myelomprotein Nle),
 Igen Primerstruktur.
 A:Reference number: A91668; MUID:77070269
 A:Contents: myeloma protein Nle
 A:Accession: B91668
 A:Molecule type: Protein
 A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'V', 242-268, 'E', 27
 A:Note: this sequence has the Gln(17) and Gln(1) markers
 R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
 Hoppe-Sejler's Z. Physiol. Chem. 364, 713-747, 1983
 A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO1
 A:Reference number: A91723; MUID:83289131
 A:Contents: myeloma protein KO1; disulfide bonds
 A:Accession: A91723
 A:Molecule type: Protein
 A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'W', 242-266, 'D', 268-271, 'D', 273-330 <SCH
 A:Note: this sequence has the Gln(3) and Gln(non-1) markers
 R:Gall, W.E.; Edelman, G.M.
 Biochemistry 9, 3188-3196, 1970
 A:Title: The covalent structure of a human gammag-immunoglobulin. X. Intrachain disulfid
 A:Reference number: A90565; MUID:71064027
 A:Contents: annotation; disulfide bonds
 R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
 Hoppe-Sejler's Z. Physiol. Chem. 357, 1515-1540, 1976
 A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
 embryonic cleavage products, and the disulfide bridges.
 A:Reference number: A91667; MUID:77070267
 A:Contents: annotation; disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG1
 A:Cross-references: GDB:120085; OMTM:147100
 A:Map position: 14q32.3-14q32.33
 A:introns: 99/1, 114/1, 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F:20-85/Domain: immunoglobulin homology <IM1> F:137-206/Domain: immunoglobulin homology <IM2> F:243-310/Domain: immunoglobulin homology <IM3> F:27-83,144-204,250-308/Disulfide bonds: #status experimental F:103/Disulfide bonds: interchain (to light chain) #status experimental F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental F:130/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.9%; Score 1233; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.3e-71;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKTHTCPPCPAPBELLGSGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMVVD 61
 DB 104 DKTHTCPPCPAPBELLGSGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMVVD 163
 QY 62 GVEVNAKTKPREQYNSTYRVSVLYVLDHWDVNGKPKCKVSNKALPAPIEKTISSAK 121
 DB 164 GVEVNAKTKPREQYNSTYRVSVLYVLDHWDVNGKPKCKVSNKALPAPIEKTISSAK 223
 QY 122 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPDSDAVEMESNGQPENNKKTTPPVLD 181
 DB 224 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPDSDAVEMESNGQPENNKKTTPPVLD 283
 QY 182 DGSFELYSKLTVDKSRMOQGVFSCSVNHEALHNHYTQKSLSISPGK 228
 DB 284 DGSFELYSKLTVDKSRMOQGVFSCSVNHEALHNHYTQKSLSISPGK 330

RESULT 3
 S69339
 Ig heavy chain V region precursor - human
 C:Species: Homo sapiens (man)
 C:Dates: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text, change 17-Mar-2000
 C:Accession: S69339
 R:Khamilich, A.A.; Auncouturier, P.; Preud'homme, J.L.; Cogne, M.
 Eur. J. Biochem. 229, 54-60, 1995
 A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
 A:Reference number: S69339; MUID:95262687
 A:Accession: S69339
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <KHA>
 A:Cross-references: EMBL:X81695
 C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 54.6%; Score 1227; DB 2; Length 374;
 Best Local Similarity 99.1%; Pred. No. 3.5e-71;
 Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DKTHTCPPCPAPBELLGSGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMVVD 61
 DB 148 DKTHTCPPCPAPBELLGSGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMVVD 207
 QY 62 GVEVNAKTKPREQYNSTYRVSVLYVLDHWDVNGKPKCKVSNKALPAPIEKTISSAK 121
 DB 208 GVEVNAKTKPREQYNSTYRVSVLYVLDHWDVNGKPKCKVSNKALPAPIEKTISSAK 267
 QY 122 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPDSDAVEMESNGQPENNKKTTPPVLD 181
 DB 268 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPDSDAVEMESNGQPENNKKTTPPVLD 327
 QY 182 DGSFELYSKLTVDKSRMOQGVFSCSVNHEALHNHYTQKSLSISPGK 228
 DB 328 DGSFELYSKLTVDKSRMOQGVFSCSVNHEALHNHYTQKSLSISPGK 374

RESULT 4
S72664
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C:Accession: S72664
R:Khamlich, A.A. EMBL Data Library, September 1994
Submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X61695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 54.6%; Score 1227; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 3.5e-71;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

2 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNMYVD 61
|||||
148 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNMYVD 207
|||||

62 GVEVHNNAKTRPREQYNSTRYVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 121
|||||

208 GVEVHNNAKTRPREQYNSTRYVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 267
|||||

122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLD 181
|||||

268 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLD 327
|||||

182 DGSFELYSLTVDKSRWQGNVFCQVMEHALNHNHTQKSLSPGK 228
|||||

328 DGSFELYSLTVDKSRWQGNVFCQVMEHALNHNHTQKSLSPGK 374
|||||

RESULT 5
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Brilich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28: 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716
Accession: PT0207
Molecule type: mRNA
Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 52.5%; Score 1180; DB 2; Length 234;
Best Local Similarity 98.6%; Pred. No. 2.1e-68;
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

2 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNMYVD 61
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15 DHTHTCPCPAPELLGGPSVFLFPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNMYVD 74
|||||

62 GVEVHNNAKTRPREQYNSTRYVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 121
|||||

75 GVEVHNNAKTRPREQYNSTRYVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 134
|||||

122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLD 181
|||||

135 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLD 194
|||||

182 DGSFELYSLTVDKSRWQGNVFCQVMEHALNHNHTQKSLSPGK 221
|||||

DB 195 DGSFELYSLTVDKSRWQGNVFCQVMEHALNHNHTQKSLSPGK 234
|||||

RESULT 6
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene.
A:Reference number: A23511; MUID:86148507
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Insertions: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 51.0%; Score 1146; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 5e-66;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

2 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNMYVD 61
|||||

151 DTPPCPCPCAPELLGGPSVFLFPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNMYVD 210
|||||

62 GVEVHNNAKTRPREQYNSTRYVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 121
|||||

211 GVEVHNNAKTRPREQYNSTRYVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 270
|||||

122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLD 181
|||||

271 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLD 330
|||||

182 DGSFELYSLTVDKSRWQGNVFCQVMEHALNHNHTQKSLSPGK 228
|||||

331 DGSFELYSLTVDKSRWQGNVFCQVMEHALNHNHTQKSLSPGK 377
|||||

RESULT 7
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb, b1, c3, c5, u) with an IGHG4 con
A:Reference number: A60764; MUID:90007613
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.9%; Score 1144; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 6.7e-66;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

2 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNMYVD 61
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Db 151 DTPPCPCPCPABELLGSGSVLEFPKPKDTLMISTPEVTCVVDVSHEDPEVKRWYD 210
Qy 62 GVEVNAKTRPREQYNSYRVSVLTVLHODMLNGEKCKVSKALPAPIEKTISKAK 121
Db 211 GVEVNAKTRPREQYNSYRVSVLTVLHODMLNGEKCKVSKALPAPIEKTISKAK 270
Qy 122 GQRPQYVTLTPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLD 181
Db 271 GQRPQYVTLTPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLD 330
Qy 182 DGSFYLTKLTVKSRMOQGNVFCSCVMHEALHNHTOKSLSPGK 228
Db 331 DGSFYLTKLTVKSRMOQGNVFCSCVMHEALHNHTOKSLSPGK 377

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RESULT 8

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G4HU gamma-2 chain C region - human
Species: Homo sapiens (man)
C>Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C/Accession: A93906; A92809; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A>Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A/Reference number: A93906; MUID:82197621
A/Accession: A93906
A/Molecule type: DNA
A/Residues: 1-326 <ELL>
A/Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A/Reference number: A92809; MUID:81007873
A/Contents: myeloma protein t11
A/Accession: A92809
A/Molecule type: Protein
A/Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A/Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A>Title: The amino acid sequences of the three heavy chain constant region domains of a
A/Reference number: A90752; MUID:80001357
A/Contents: myeloma protein z1e
A/Accession: A90752
A/Molecule type: Protein
A/Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A/Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A/Reference number: A93132; MUID:80114419
A/Contents: z1e
A/Accession: A93132
A/Molecule type: protein
A/Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A/Reference number: A94591
A/Contents: annotation; z1e, revisions to residues 25, 59, 60, and 264-268
A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A>Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A/Reference number: A90253; MUID:72033500
A/Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A>Title: Structural studies of immunoglobulin G.
A/Reference number: A93157; MUID:69064124
A/Contents: annotation; Sa, disulfide bonds
C/Genetics:

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A/Gene: GDB:IGHG2
A/Cross-references: GDB:119338; OMIM:147110
A/Map position: 14q32.33-14q32.33
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:135-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match 50.9%; Score 1142.5; DB 1; Length 326;
Best Local Similarity 94.1%; Pred. No. 7,2e-66;
Matches 209; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

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Qy 7 CPGCPAPELGSPVLEFPKPKDTLMISTPEVTCVVDVSHEDPEVKRWYDGYEVH 66
Db 106 CPGCPAPP-VAGPSVLEFPKPKDTLMISTPEVTCVVDVSHEDPEVQFMWYDGYEVH 164
Qy 67 NAKTRPREQYNSYRVSVLTVLHODMLNGEKCKVSKALPAPIEKTISKAGOPRE 126
Db 165 NAKTRPREQYNSYRVSVLTVLHODMLNGEKCKVSKALPAPIEKTISKAGOPRE 224
Qy 127 POYVTLTPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFF 186
Db 225 POYVTLTPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFF 284
Qy 187 LYSKLTVDKSRMOQGNVFCSCVMHEALHNHTOKSLSPGK 228
Db 285 LYSKLTVDKSRMOQGNVFCSCVMHEALHNHTOKSLSPGK 326

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RESULT 9

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G4HU Ig gamma-4 chain C region - human
Species: Homo sapiens (man)
C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C/Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A>Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A/Reference number: A90933; MUID:83157104
A/Accession: A90933
A/Molecule type: DNA
A/Residues: 1-327 <ELL>
A/Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A>Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constan
A/Reference number: A90249; MUID:70207560
A/Accession: A90249
A/Molecule type: protein
A/Residues: 1-30;81-326 <PIN>
C/Genetics:
A/Gene: GDB:IGHG4
A/Cross-references: GDB:119340; OMIM:147130
A/Map position: 14q32.33-14q32.33
A/Introns: 99/1, 111/1, 221/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:53:56 ; Search time 27.53 Seconds
(without alignments)
244.142 Million cell updates/sec

Title: US-09-389-545-8

Perfect score: 2246

Sequence: 1 MDKHTCPCPAPPELLGSPS.....QKGNATHDNCISGNSSEK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

al number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/3A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
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5: /cgn2_6/ptodata/2/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1234 | 54.9 | 347 | 1 | US-07-940-861-43 Sequence 43, Appl |
| 2 | 1234 | 54.9 | 347 | 1 | US-08-459-512-43 Sequence 43, Appl |
| 3 | 1234 | 54.9 | 347 | 2 | US-08-459-657-43 Sequence 43, Appl |
| 4 | 1234 | 54.9 | 347 | 2 | US-08-460-132-43 Sequence 43, Appl |
| 5 | 1234 | 54.9 | 347 | 4 | PCT-US92-02050-43 Sequence 43, Appl |
| 6 | 1233 | 54.9 | 323 | 2 | US-08-595-043A-50 Sequence 50, Appl |
| 7 | 1233 | 54.9 | 371 | 1 | US-08-236-311-7 Sequence 7, Appl |
| 8 | 1233 | 54.9 | 371 | 3 | US-08-457-918-7 Sequence 7, Appl |
| 9 | 1233 | 54.9 | 387 | 1 | US-08-470-299-4 Sequence 4, Appl |
| 10 | 1233 | 54.9 | 396 | 2 | US-08-784-512-3 Sequence 3, Appl |
| 11 | 1233 | 54.9 | 424 | 4 | PCT-US95-03866-12 Sequence 12, Appl |
| 12 | 1233 | 54.9 | 424 | 4 | PCT-US95-03866-14 Sequence 14, Appl |
| 13 | 1233 | 54.9 | 437 | 4 | PCT-US96-10043-11 Sequence 11, Appl |
| 14 | 1233 | 54.9 | 442 | 4 | PCT-US96-10043-9 Sequence 9, Appl |
| 15 | 1233 | 54.9 | 449 | 1 | US-08-458-516-13 Sequence 13, Appl |
| 16 | 1233 | 54.9 | 459 | 1 | US-08-157-101A-7 Sequence 7, Appl |
| 17 | 1233 | 54.9 | 476 | 2 | US-08-378-939-10 Sequence 10, Appl |
| 18 | 1233 | 54.9 | 476 | 3 | US-08-487-550-4 Sequence 4, Appl |
| 19 | 1233 | 54.9 | 476 | 3 | US-08-487-550-12 Sequence 12, Appl |
| 20 | 1233 | 54.9 | 478 | 3 | US-08-487-550-8 Sequence 8, Appl |
| 21 | 1238 | 54.7 | 254 | 3 | US-08-284-391B-33 Sequence 33, Appl |
| 22 | 1228 | 54.7 | 664 | 3 | US-08-957-063-16 Sequence 16, Appl |
| 23 | 1228 | 54.7 | 664 | 3 | US-08-957-063-18 Sequence 18, Appl |
| 24 | 1227 | 54.6 | 449 | 3 | US-08-897-336-23 Sequence 23, Appl |
| 25 | 1227 | 54.6 | 451 | 2 | US-08-887-352B-14 Sequence 14, Appl |
| 26 | 1227 | 54.6 | 451 | 2 | US-08-887-352B-16 Sequence 16, Appl |
| 27 | 1227 | 54.6 | 451 | 2 | US-08-887-352B-18 Sequence 18, Appl |
| 28 | 1227 | 54.6 | 451 | 3 | US-08-466-151-65 Sequence 65, Appl |

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|----|--------|------|-----|---|--|
| 29 | 1227 | 54.6 | 452 | 3 | US-09-027-449-71 Sequence 71, Appl |
| 30 | 1227 | 54.6 | 453 | 3 | US-08-466-151-8 Sequence 8, Appl |
| 31 | 1227 | 54.6 | 454 | 2 | US-07-934-373C-22 Sequence 22, Appl |
| 32 | 1227 | 54.6 | 454 | 3 | US-08-437-642B-22 Sequence 22, Appl |
| 33 | 1227 | 54.6 | 454 | 4 | PCT-US93-07832-22 Sequence 22, Appl |
| 34 | 1224 | 54.5 | 911 | 2 | US-08-484-438-10 Sequence 10, Appl |
| 35 | 1221 | 54.4 | 442 | 1 | US-08-461-968A-5 Sequence 5, Appl |
| 36 | 1221 | 54.4 | 442 | 2 | US-08-462-571-5 Sequence 5, Appl |
| 37 | 1216.5 | 54.2 | 486 | 1 | US-08-243-010-1 Sequence 1, Appl |
| 38 | 1216.5 | 54.2 | 552 | 1 | US-08-243-010-6 Sequence 6, Appl |
| 39 | 1215 | 54.1 | 438 | 1 | US-06-097-827-11 Sequence 11, Appl |
| 40 | 1215 | 54.1 | 438 | 1 | US-08-494-574-11 Sequence 11, Appl |
| 41 | 1212 | 54.0 | 232 | 1 | US-07-797-556-4 Sequence 4, Appl |
| 42 | 1212 | 54.0 | 232 | 1 | US-08-225-989-4 Sequence 4, Appl |
| 43 | 1212 | 54.0 | 232 | 1 | US-08-570-923-4 Sequence 4, Appl |
| 44 | 1212 | 54.0 | 232 | 1 | US-08-580-014-4 Sequence 4, Appl |
| 45 | 1212 | 54.0 | 232 | 4 | PCT-US95-06530-4 Sequence 4, Appl |

ALIGNMENTS

RESULT 1
US-07-940-861-43
; Sequence 43, Application US/07940861
; Patent No. 5547853
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07940,861
; FILING DATE: 21-OCT-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: 3151C1P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ. ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-07-940-861-43

Query Match 54.9%; Score 1234; DB 1; Length 347;
Best Local Similarity 99.6%; Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKHTPCPCAPAPLGGPSVFLFPKPKDTLMSRTEPYTCVYVDVSHDEPEVKFNMVY 60
DB 120 VDKHTPCPCAPAPLGGPSVFLFPKPKDTLMSRTEPYTCVYVDVSHDEPEVKFNMVY 179
QY 61 DGEVHNKAKTRPEQYNSYTRVSVLTVLHODMLNGEKYCKVSNKALPAPIETISKA 120
DB 180 DGEVHNKAKTRPEQYNSYTRVSVLTVLHODMLNGEKYCKVSNKALPAPIETISKA 239
QY 121 KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTPPVLD 180
DB 240 KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTPPVLD 299
181 SDGSFELYSKLTVDKSRMOGNFSCVMHEALHNHYTKSLSPGK 228
DB 300 SDGSFELYSKLTVDKSRMOGNFSCVMHEALHNHYTKSLSPGK 347

RESULT 2

US-08-459-512-43
Sequence 43, Application US/08459512
Patent No. 5728677
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: MILLER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,512
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B15ICIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-459-512-43

Query Match 54.9%; Score 1234; DB 1; Length 347;
Best Local Similarity 99.6%; Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKHTPCPCAPAPLGGPSVFLFPKPKDTLMSRTEPYTCVYVDVSHDEPEVKFNMVY 60
DB 120 VDKHTPCPCAPAPLGGPSVFLFPKPKDTLMSRTEPYTCVYVDVSHDEPEVKFNMVY 179
QY 61 DGEVHNKAKTRPEQYNSYTRVSVLTVLHODMLNGEKYCKVSNKALPAPIETISKA 120
DB 180 DGEVHNKAKTRPEQYNSYTRVSVLTVLHODMLNGEKYCKVSNKALPAPIETISKA 239
QY 121 KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTPPVLD 180
DB 240 KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVEMESNGOPENNYKTPPVLD 299
181 SDGSFELYSKLTVDKSRMOGNFSCVMHEALHNHYTKSLSPGK 228
DB 300 SDGSFELYSKLTVDKSRMOGNFSCVMHEALHNHYTKSLSPGK 347

RESULT 3

US-08-459-657-43
Sequence 43, Application US/08459657
Patent No. 5914111
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: MILLER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,657
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B15ICIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-657-43

Query Match 54.9%; Score 1234; DB 2; Length 347;
Best Local Similarity 99.6%; Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCPAPAPELLGGSVFLEPPPKDITLMSRTEVTCVVDVSHDEPEKFMWY 60
DB 120 VDKTHCPAPAPELLGGSVFLEPPPKDITLMSRTEVTCVVDVSHDEPEKFMWY 179
QY 61 DGEVHNAKTRPREQNSTYRVSVLTVLHODMLNGKEYCKVSKALPALEKITSKA 120
DB 180 DGEVHNAKTRPREQNSTYRVSVLTVLHODMLNGKEYCKVSKALPALEKITSKA 239
QY 121 KGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPPVLD 180
DB 240 KGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPPVLD 299
181 SDGSFLYSKLTVDKSRMOGQNFSCVMHEALHNHYTOKSLSLSPGK 228
DB 300 SDGSFLYSKLTVDKSRMOGQNFSCVMHEALHNHYTOKSLSLSPGK 347

RESULT 4
US-08-460-132-43
Sequence 43, Application US/08460132
Patent No. 5928643

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,132
CLASSIFICATION: 424
FILING DATE: 02-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,861
FILING DATE: 21-OCT-1992
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-132-43

Query Match 54.9%; Score 1234; DB 2; Length 347;
Best Local Similarity 99.6%; Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCPAPAPELLGGSVFLEPPPKDITLMSRTEVTCVVDVSHDEPEKFMWY 60
DB 120 VDKTHCPAPAPELLGGSVFLEPPPKDITLMSRTEVTCVVDVSHDEPEKFMWY 179
QY 61 DGEVHNAKTRPREQNSTYRVSVLTVLHODMLNGKEYCKVSKALPALEKITSKA 120
DB 180 DGEVHNAKTRPREQNSTYRVSVLTVLHODMLNGKEYCKVSKALPALEKITSKA 239
QY 121 KGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPPVLD 180
DB 240 KGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOPENNYKTPPVLD 299
181 SDGSFLYSKLTVDKSRMOGQNFSCVMHEALHNHYTOKSLSLSPGK 228
DB 300 SDGSFLYSKLTVDKSRMOGQNFSCVMHEALHNHYTOKSLSLSPGK 347

RESULT 5
PCT-US92-02050-43

Sequence 43, Application PC/TUS9202050

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 19920312
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:

LENGTH: 347 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-02050-43

Query Match 54.9%: Score 1234; DB 4; Length 347;
Best Local Similarity 99.6%: Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVFNMYV 60
Db 120 VDKTTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVFNMYV 179
Db 61 DGEVHNNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120
Db 180 DGEVHNNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 239
Db 121 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
Qy 240 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 299
Qy 181 SDGSFELSKLTVDKSRMQQGVNFCISYMHREALHNHTYOKSLSLSPGK 228
Db 300 SDGSFELSKLTVDKSRMQQGVNFCISYMHREALHNHTYOKSLSLSPGK 299

RESULT 6
US-08-595-043A-50
Sequence 50, Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-50.

Query Match 54.9%: Score 1233; DB 2; Length 232;
Best Local Similarity 100.0%: Pred. No. 8.3e-86;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVFNMYV 61

Db 6 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVFNMYV 65
Qy 62 GVEVHNNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 66 GVEVHNNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 125
Qy 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 181
Db 126 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 185
Qy 182 DGSFELSKLTVDKSRMQQGVNFCISYMHREALHNHTYOKSLSLSPGK 228
Db 186 DGSFELSKLTVDKSRMQQGVNFCISYMHREALHNHTYOKSLSLSPGK 232

RESULT 7
US-08-236-311-7
Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adhesion Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-236-311-7

Query Match 54.9%: Score 1233; DB 1; Length 371;
Best Local Similarity 100.0%: Pred. No. 1.6e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTGCPAPAPLGGPSVFLFPPKPKDTLMTSRTPEVTCVVVDVSHEDPEVKFNNYVD 61
Db 145 DKHTGCPAPAPLGGPSVFLFPPKPKDTLMTSRTPEVTCVVVDVSHEDPEVKFNNYVD 204
QY 62 GVEVHNAKTRPREQYNSTRYVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 121
Db 205 GVEVHNAKTRPREQYNSTRYVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 264
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181
Db 265 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 324
QY 182 DGSFELSKLTVDKSRWQGQVNFSCSYMHENLHNHYTQKSLSLSPGK 228
Db 325 DGSFELSKLTVDKSRWQGQVNFSCSYMHENLHNHYTQKSLSLSPGK 371

RESULT 8

US-08-457-918-7
Sequence 7, Application US/08457918
Patent No. 6117635

GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adhesion Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/2250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104323
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kudinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-457-918-7

Query Match 54.9%; Score 1233; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTGCPAPAPLGGPSVFLFPPKPKDTLMTSRTPEVTCVVVDVSHEDPEVKFNNYVD 61
Db 145 DKHTGCPAPAPLGGPSVFLFPPKPKDTLMTSRTPEVTCVVVDVSHEDPEVKFNNYVD 204
QY 62 GVEVHNAKTRPREQYNSTRYVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 121
Db 205 GVEVHNAKTRPREQYNSTRYVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 264
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181
Db 265 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 324
QY 182 DGSFELSKLTVDKSRWQGQVNFSCSYMHENLHNHYTQKSLSLSPGK 228
Db 325 DGSFELSKLTVDKSRWQGQVNFSCSYMHENLHNHYTQKSLSLSPGK 371

RESULT 9

US-08-470-299-4
Sequence 4, Application US/08470299
Patent No. 5783181

GENERAL INFORMATION:

APPLICANT: Browne, Michael J.
APPLICANT: Murphy, Kay E.
APPLICANT: Chapman, Conrad G.
APPLICANT: Clinkbeard, Helen E.
APPLICANT: Young, Peter R.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P31005C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-470-299-4

Query Match 54.9%; Score 1233; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTGCPAPAPLGGPSVFLFPPKPKDTLMTSRTPEVTCVVVDVSHEDPEVKFNNYVD 61
Db 161 DKHTGCPAPAPLGGPSVFLFPPKPKDTLMTSRTPEVTCVVVDVSHEDPEVKFNNYVD 220

QY 62 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIETISKAK 121
| | | | |
Db 221 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIETISKAK 280
QY 122 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQENNYKTTTPVYLS 181
| | | | |
Db 281 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQENNYKTTTPVYLS 340
QY 182 DGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 228
| | | | |
Db 341 DGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 387

RESULT 10
US-08-784-512-3

; Sequence 3, Application US/08784512
; Patent No. 5872209
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BOETTNER, Frank
; APPLICANT: CATERSON, Bruce
; APPLICANT: HUGHES, Clare
; TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
; TITLE OF INVENTION: And native aggregan to study the proteolytic activity of
; TITLE OF INVENTION: "aggreganase" in cell culture systems
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,512
; FILING DATE: 17-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96100682.2
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REFERENCE/DOCKET NUMBER: 33,683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..396
; US-08-784-512-3

Query Match 54.9%; Score 1233; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 1,7e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 61
| | | | |
Db 170 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 229

QY 62 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIETISKAK 121
| | | | |
Db 230 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIETISKAK 289
QY 122 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQENNYKTTTPVYLS 181
| | | | |
Db 290 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQENNYKTTTPVYLS 349
QY 182 DGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 228
| | | | |
Db 350 DGSFELYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 396

RESULT 11
PCT-US95-03866-12

; Sequence 12, Application PC/TUS9503866
; GENERAL INFORMATION:
; APPLICANT: Cytomed, Inc. (all states except US)
; APPLICANT: Nocka, Karl (US only)
; APPLICANT: Lobell, Robert B (US only)
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,379
; FILING DATE: 28-MAR-1994;
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Cytomed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9090
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-03866-12

Query Match 54.9%; Score 1233; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.9e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 61
| | | | |
Db 198 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 257
QY 62 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIETISKAK 121
| | | | |
Db 258 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIETISKAK 317
QY 122 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQENNYKTTTPVYLS 181
| | | | |

DB 318 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 377
QY 182 DGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 378 DGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 424

RESULT 12

PCT-US95-03866-14
; Sequence 14, Application PC/TUS9503866
; GENERAL INFORMATION:
; APPLICANT: CytoMed, Inc. (all states except US)
; APPLICANT: Nocke, Karl (US only)
; APPLICANT: Lobell, Robert B (US only)
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,379
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: CytoMed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
-US95-03866-14

Query Match 54.9%; Score 1233; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 1,9e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTGCPAPAPLLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVD 61
DB 198 DKHTGCPAPAPLLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVD 257
QY 62 GVVVHNAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAK 121
DB 258 GVVVHNAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAK 317
QY 122 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 181
DB 318 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 377
QY 182 DGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 378 DGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 424

RESULT 13

PCT-US96-10043-11
; Sequence 11, Application PC/TUS9610043
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10043
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,213
; FILING DATE: 14-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lecht, Karen F.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 00786/284001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10043-11

Query Match 54.9%; Score 1233; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTGCPAPAPLLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVD 61
DB 211 DKHTGCPAPAPLLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVD 270
QY 62 GVVVHNAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAK 121
DB 271 GVVVHNAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAK 330
QY 122 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 181
DB 331 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 390
QY 182 DGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 391 DGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 437

RESULT 14

PCT-US96-10043-9
; Sequence 9, Application PC/TUS9610043
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES

TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-9

Query Match 54.9%; Score 1233; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTCPPCPAPELLGSGSVFLPPKPKDITLMSITPREVTCVVDVSHEDPEVKFNMYD 61
DB 216 DKHTCPPCPAPELLGSGSVFLPPKPKDITLMSITPREVTCVVDVSHEDPEVKFNMYD 275
QY 62 GVEVHNNAKTRPREQYNSTYRVSVLTVLHODWLNKREYCKVSNKALPAPIEKTISKAK 121
DB 276 GVEVHNNAKTRPREQYNSTYRVSVLTVLHODWLNKREYCKVSNKALPAPIEKTISKAK 335
QY 122 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDS 181
DB 336 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDS 395
QY 182 DGSFELYSKLTVDKSRMOQGVFSCVMHEALHNHYTOKSLISPGK 228
DB 396 DGSFELYSKLTVDKSRMOQGVFSCVMHEALHNHYTOKSLISPGK 442

RESULT 15
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith

STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 54.9%; Score 1233; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTCPPCPAPELLGSGSVFLPPKPKDITLMSITPREVTCVVDVSHEDPEVKFNMYD 61
DB 223 DKHTCPPCPAPELLGSGSVFLPPKPKDITLMSITPREVTCVVDVSHEDPEVKFNMYD 282
QY 62 GVEVHNNAKTRPREQYNSTYRVSVLTVLHODWLNKREYCKVSNKALPAPIEKTISKAK 121
DB 283 GVEVHNNAKTRPREQYNSTYRVSVLTVLHODWLNKREYCKVSNKALPAPIEKTISKAK 342
QY 122 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDS 181
DB 343 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDS 402
QY 182 DGSFELYSKLTVDKSRMOQGVFSCVMHEALHNHYTOKSLISPGK 228
DB 403 DGSFELYSKLTVDKSRMOQGVFSCVMHEALHNHYTOKSLISPGK 449

Search completed: December 27, 2000, 10:53:58
Job time: 149 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:53:25 ; Search time 40.04 Seconds

(without alignments)
342.450 Million cell updates/sec

Title: US-09-389-545-8

Sequence: 1 MDKTHTCPPCPAPELLGGS.....QKGNATHDNICSGNSESTQK 401

Scoring table: BLOSUM62

Searched: 268485 seqs, 34193795 residues

total number of hits satisfying chosen parameters: 268485

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%

Database : A_Geneseq_36:★

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|--------|--------------------|
| 1 | 1239.5 | 55.2 | 652 | 19 | W48650 | Heavy chain of hma |
| 2 | 1238 | 55.1 | 374 | 19 | M83963 | Recombinant human |
| 3 | 1238 | 55.1 | 374 | 19 | W49075 | Recombinant human |
| 4 | 1237 | 55.1 | 235 | 20 | Y01372 | Amino acid sequenc |
| 5 | 1236.5 | 55.1 | 651 | 18 | M26648 | Chimeric receptor |
| 6 | 1236.5 | 55.1 | 652 | 18 | M26650 | Chimeric receptor |
| 7 | 1234 | 54.9 | 347 | 13 | R27163 | CD2 binding LFA-3 |
| 8 | 1234 | 54.9 | 347 | 21 | Y83136 | Human transmembran |
| 9 | 1234 | 54.9 | 388 | 19 | W33513 | Rabbit TGFbetaRII |
| 10 | 1234 | 54.9 | 388 | 19 | Y73514 | Human TGFbetaRII.F |
| 11 | 1234 | 54.9 | 388 | 21 | Y54063 | Amino acid sequenc |
| 12 | 1234 | 54.9 | 388 | 21 | Y54064 | Amino acid sequenc |

| | | | | | | |
|----|------|------|-----|----|--------|---------------------|
| 13 | 1234 | 54.9 | 339 | 21 | Y70867 | Human interferon-b |
| 14 | 1234 | 54.9 | 418 | 21 | Y70868 | Human interferon-b |
| 15 | 1234 | 54.9 | 423 | 21 | Y70869 | Human interferon-b |
| 16 | 1234 | 54.9 | 446 | 15 | R58753 | VCAM 2D-19g, Homo |
| 17 | 1234 | 54.9 | 446 | 20 | Y23986 | VCAM 2D-19g, a sol |
| 18 | 1234 | 54.9 | 446 | 20 | Y01037 | VCAM 2D-19g protei |
| 19 | 1234 | 54.9 | 446 | 20 | W96743 | A VCAM 2D-19g1 fus |
| 20 | 1234 | 54.9 | 482 | 19 | W31646 | Human cytokine rec |
| 21 | 1233 | 54.9 | 232 | 18 | W62632 | Human IgG1 hinge/F |
| 22 | 1233 | 54.9 | 233 | 20 | Y06617 | Human IgG1 hinge/F |
| 23 | 1233 | 54.9 | 259 | 20 | Y24354 | Human Fc (IgG1) |
| 24 | 1233 | 54.9 | 329 | 17 | R91806 | Protein from pcd51 |
| 25 | 1233 | 54.9 | 351 | 14 | R43685 | Human immunoglobul |
| 26 | 1233 | 54.9 | 371 | 10 | P91918 | Human kappa immuno |
| 27 | 1233 | 54.9 | 371 | 10 | P93558 | Sequence of the li |
| 28 | 1233 | 54.9 | 376 | 19 | W60037 | Linked human IgG |
| 29 | 1233 | 54.9 | 379 | 19 | W83962 | Antigenic peptide |
| 30 | 1233 | 54.9 | 379 | 19 | W49073 | Recombinant human |
| 31 | 1233 | 54.9 | 379 | 19 | W49074 | Recombinant human |
| 32 | 1233 | 54.9 | 387 | 17 | R90920 | Recombinant human |
| 33 | 1233 | 54.9 | 396 | 18 | W18574 | IL4, Y144D/IgG1 pro |
| 34 | 1233 | 54.9 | 396 | 18 | W18575 | Aggrecanase activi |
| 35 | 1233 | 54.9 | 400 | 21 | Y15123 | Aggrecanase artif |
| 36 | 1233 | 54.9 | 424 | 16 | W14764 | Porcine CTLA-4-Ig |
| 37 | 1233 | 54.9 | 424 | 16 | W14765 | Human soluble kit |
| 38 | 1233 | 54.9 | 435 | 13 | R26530 | Human soluble kit |
| 39 | 1233 | 54.9 | 437 | 18 | W10552 | Sequence of one ch |
| 40 | 1233 | 54.9 | 442 | 18 | W10550 | Alpha1-acid glyco |
| 41 | 1233 | 54.9 | 445 | 20 | Y24153 | IgG1 polypeptide. |
| 42 | 1233 | 54.9 | 446 | 17 | W05829 | Bovine LOX-1 extra |
| 43 | 1233 | 54.9 | 447 | 20 | Y31669 | Humanised Id10 ant |
| 44 | 1233 | 54.9 | 449 | 14 | R43639 | Human IgG1 chain C |
| 45 | 1233 | 54.9 | 449 | 19 | W43616 | Human IgG1 chain C |
| | | | | | | Completely humanis |
| | | | | | | Amino acid sequenc |

ALIGNMENTS

| RESULT | 1 |
|--------|---|
| XX | W48650 |
| XX | ID W48650 standard; Protein; 652 AA. |
| XX | AC W48650; |
| XX | DT |
| XX | 04-AUG-1998 (first entry) |
| XX | Heavy chain of hmab425 fused to TNF alpha. |
| XX | XX |
| XX | Antibody-cytokine fusion protein; tristicronic vector; chimeric |
| XX | TNF alpha; IL-2; IRES; internal ribosome entry site. |
| XX | OS Synthetic. |
| XX | OS Homo sapiens. |
| XX | Key |
| XX | Location/Qualifiers |
| XX | FT Region 1..494 "Heavy chain of human mab 425" |
| XX | FT Region 495..652 |
| XX | FT Region /note="TNF alpha" |
| XX | PN W09811241-A1. |
| XX | PD 19-MAR-1998. |
| XX | PE 02-SEP-1997; 97WO-EP04765. |
| XX | PR 30-SEP-1996; 96EP-0115635. |
| XX | PR 16-SEP-1996; 96EP-0114820. |
| XX | PA (MERE) MERCK PATENT GMBH. |
| XX | Brummer W, Burge C, Dunker R, Hauser H, Mielke C; |
| XX | Rieke E, Von Hoegen I, Weijge T; |

XX WPI: 1998-207400/18.
 DR N-PSDB; V18096.
 DR Oligo: cistronic expression vector - useful for production of, e.g.
 PT MAb425/TNF- α or MAb425/IL-2 antibody fusion protein
 PT MAb425/TNF- α or MAb425/IL-2 antibody fusion protein
 XX Disclosure: Fig 15; 89pp; English.
 XX The present sequence represents a fusion protein comprising of TNF
 CC alpha fused to the C-terminus of the heavy chain of the human
 CC monoclonal antibody 425 (ImAb425). The ImAb425 has specificity for
 CC the human EGF receptor. The invention claims for a new monoclonal
 CC trivalent vector (V18096) for the expression of an antibody-cytokine
 CC fusion protein, ImAb425-TNF alpha. The TNF alpha sequence can be
 CC substituted by the IL-2 sequence. The vector also contains a strong
 CC promoter/enhancer unit, a selection marker gene and at least two
 CC poliovirus derived internal ribosomal entry site (IRES) sequences. The
 CC vector can be expressed in mammalian host cells for the production of
 CC heteromeric fusion proteins. This expression system is claimed to
 CC produce the heteromeric proteins in high yields.

XX Sequence 652 AA;

Query Match 55.2%; Score 1239.5; DB 19; Length 652;
 Best Local Similarity 65.8%; Pred. No. 9,4e-76;
 Matches 250; Conservative 19; Mismatches 54; Indels 57; Gaps 6;

OY 2 DKTHPCPCPAPPELLGSPVFLPPPKPKDLMISRTPEVTCVYVDVSHEDPEVKFMVYD 61
 DB dkthcpcpcpapellgspvflfpkpkdltmistrpevcvvdvshedpevkfmvdy 327
 OY 62 GVEVHNKATPREEQVNSTYRVSVLTVLHODWLNGKEYCKVSKALPAPIEKTISKAK 121
 DB gvevhnaktpreeqvnslyrvsvltvlhqdwlngkeyckvskalpapiektiskak 387
 OY 122 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPDIAVMEESNGOPENNYKTTTPVYLD 181
 DB gqprepqvylppsrdeltknqvsltcclvkgfypsdiavmesngopennnyktctppvld 447
 OY 182 DGSFFLYSKLTVDKSRWQGNVFSVMEALHNHYTKQSLSPGKETFPKRYLHYDEE 241
 DB dgsfflyskltvdksrwqgnvfscvmealhnhytkqslspgkmtfprkrylhydes 507
 OY 242 TSHQLCDKCPPEGYTLKHQHTAKMTVCAPCPDHYTDSMHTSDCLYSPVCK-ELQTV 300
 DB tshqlcdkcppegytlkhqhtakmtvcapcpdhyttdsmhtsdclyspvck-elotv 524
 OY 301 KOECNR-----THNRYCECKEGRYL-EIEFCLKHRSRCPGFVYQAGTPEKNTVCKR 351
 DB 555 nrraallaangvelndnglvwpseglyllysgvltkqggc-psthnllthtistravsyq 583
 OY 352 CPDGFSSNETSSKAPCRKHT 371
 DB 584 tkvnlls---alkspcqrct 600

RESULT 2

W83963 ID W83963 standard; Protein; 374 AA.

XX W83963;

XX 05-FEB-1999 (first entry)

DE Recombinant human metFc-OB protein variant.

KW Recombinant; metFc-OB protein; FC region; immunoglobulin; Ig; OB;
 KW obesity; human; adiposity; blood lipid; diabetes type II; insulin;
 KW hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
 KW suspension; variant.

OS Homo sapiens.
 XX W09846257-A1.
 XX 22-OCT-1998.
 XX 16-APR-1998; 98WO-US07828.
 XX 14-APR-1998; 98US-0059467.
 XX 17-APR-1997; 97US-0843971.
 XX (AMGE-) AMGEN INC.
 XX Brems DN, French DL, Speed MA;
 XX WPI: 1998-594525/50.
 XX N-PSDB; V69686.
 XX This represents a recombinant metFc-OB protein variant which consists of
 CC an FC region of human immunoglobulin (Ig) fused to a human OB (obesity)
 CC protein. The invention provides a human OB protein suspension that
 CC contains at least 0.5 mg/ml of the human OB protein derivatised by
 CC attachment of the FC region of an Ig to the N-terminus of OB, and has a
 CC pH 6-8. The suspensions are used to reduce weight, adiposity and blood
 CC lipid levels, to treat or prevent diabetes type II, and to increase lean
 CC mass and insulin sensitivity. They may be used in conjunction with
 CC insulin, hypoglycaemics, antihypertensives, diuretics, appetite
 CC suppressants etc. These suspensions are stable and active at
 CC physiological pH and are ready-for-use formulations that do not require
 CC freezing or freeze drying. As they are very concentrated, only small
 CC volumes are required and they provide a sustained-release effect, with
 CC increased potency and reduced frequency of injection.

Claim 2; Fig 6A-C; 47pp; English.

XX Sequence 374 AA;

Query Match 55.1%; Score 1238; DB 19; Length 374;
 Best Local Similarity 100.0%; Pred. No. 6,1e-76;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKTHPCPCPAPPELLGSPVFLPPPKPKDLMISRTPEVTCVYVDVSHEDPEVKFMVY 60
 DB 1 mdkthcpcpcpapellgspvflfpkpkdltmistrpevcvvdvshedpevkfmvy 60
 OY 61 DGEVHNKATPREEQVNSTYRVSVLTVLHODWLNGKEYCKVSKALPAPIEKTISKAK 120
 DB 61 dgevhnaktpreeqvnslyrvsvltvlhqdwlngkeyckvskalpapiektiskaka 120
 OY 121 KGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPDIAVMEESNGOPENNYKTTTPVYLD 180
 DB 121 kgprepqvylppsrdeltknqvsltcclvkgfypsdiavmesngopennnyktctppvld 180
 OY 181 SDGSFFLYSKLTVDKSRWQGNVFSVMEALHNHYTKQSLSPGKETFPKRYLHYDEE 228
 DB 181 sdgsfflyskltvdksrwqgnvfscvmealhnhytkqslspgk 228

RESULT 3

W49075 ID W49075 standard; Protein; 374 AA.

XX W49075;

XX 18-NOV-1998 (first entry)

DE Recombinant human MetFc-OB variant 2 protein.

XX XX Recombinant human MetFc-OB variant 2 protein; chimeric; immunoglobulin;
 KW high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
 KW diabetes.
 XX XX Homo sapiens.
 OS Synthetic.
 XX XX Key Location/Qualifiers
 FH 2..374
 FT Protein /note= "Recombinant human Fc-OB variant 2 protein"
 FT 229..374
 FT Region /note= "human OB protein"
 XX XX WO9828427-A1.
 XX XX 02-JUL-1998.
 PD 11-DEC-1997; 97WO-US23183.
 XX 20-DEC-1996; 96US-0770973.
 PF (AMGE-) AMGEN INC.
 PA Hecht RI, Mann MB;
 XX WPI: 1998-377658/32.
 DR N-PSDB: V32902.
 XX New fusion proteins of OB and Fc - used for treating e.g. excess
 PT weight, diabetes, arterial sclerosis, arterial plaque, high blood
 PT lipid level, gall stones or stroke
 XX Claim 2: Fig 5A-5C; 107pp; English.
 XX PS The present sequence represents a recombinant human MetFc-OB variant 2
 CC fusion protein having a 5 residue deletion of residues 2-6 of the
 CC wild-type Fc-OB protein sequence shown in W49073. The invention provides
 CC Fc-OB fusion proteins whereby the Fc region of an immunoglobulin or its
 CC analogue is linked, either directly or indirectly using a linker, to the
 CC N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
 CC are claimed to demonstrate increased stability and clearance rate and
 CC decreased degradation as compared to OB protein or a fusion of Fc to
 CC the C-terminus of the OB protein. These Fc-OB fusion proteins are also
 CC claimed to be useful for treating excess weight in an individual or
 CC animal or for treating co-morbidities associated with excess fat such as
 CC diabetes, high blood lipid level, arterial sclerosis and stroke.

Sequence 374 AA:
 Query Match 55.1%; Score 1238; DB 19; Length 374;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-76;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCPAPAPBELLGGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWY 60
 DB 1 mdkthcpapapbellggsvflfppkpkdtlmisrtpevtcvvdvshedpevkimwy 60
 QY 61 DGVEVHNAKTRPREOYNSTYRVASVLTALHODMLNGKVKCVSNKALPAPTEKTSKA 120
 DB 61 dgvevhnaktrpreoynstyrvasvltalhdwlngkvcvsnalpaplextlska 120
 QY 121 KQCPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAEWESNGCPENNYTTTPVL 180
 DB 121 kgcprepgvyltlppsrdeltkngvslclvkgfypsdiaewesngpenykttpvld 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVFCGSVMHDAIHNHTQKSLISPGK 228
 DB 181 sdgsfflyskltvdksrwqgnvfcsvmhdaiahnhtqgslispgk 228

RESULT 4

Y01372
 ID Y01372 standard; Protein: 235 AA.
 XX AC Y01372;
 XX DT 04-JUN-1999 (first entry)
 XX DE Amino acid sequence of Fc fragment of human IgG.
 XX FcRn: binding; epithelial cell; immune system; modulation; antigen;
 KW pathogen; autoimmune disease; allergen; tumour; therapeutic; cytokine;
 KW chemotherapy agent; interferon; insulin; human growth hormone; fertility;
 KW drug; calcitonin; steroid; immunity; mucosal; AIDS; hepatitis; Fc; human;
 KW immunoglobulin; 196.
 XX XX Homo sapiens.
 OS
 XX XX Key Location/Qualifiers
 FH MISC-difference 230
 FT /note= "encoded by TGA"
 XX WO9304813-A1.
 XX 04-FEB-1999.
 PD 24-JUL-1998; 98WO-US15395.
 XX 24-JUL-1997; 97US-0899856.
 XX (BGMH) BRIGHAM & WOMENS HOSPITAL.
 PA (UYBR-) UNIV BRANDEIS.
 PI Blumerg RS, Lencer WI, Simister NE;
 XX WPI: 1999-153297/13.
 DR N-PSDB: X27800.
 XX Delivering therapeutics, particularly antigens to epithelial cells -
 PT comprises use of a conjugate of the therapeutic and an FcRn binding
 PT partner
 XX PS Disclosure: Fig 1; 74pp; English.
 XX CC The invention relates to methods of delivering molecules to a mammal by
 CC administering a conjugative of a therapeutic or a bioactive substance,
 CC and an FcRn binding partner targeted to epithelial cells expressing FcRn.
 CC This can be used for modulating a mammalian immune system wherein, the
 CC bioactive substance is an antigen characteristic of a pathogen of an
 CC autoimmune disease, an allergen, or a tumour. The delivering method is
 CC used to deliver therapeutics, including chemotherapy agents, cytokines
 CC including interferon, hormones, including insulin and human growth
 CC hormone, fertility drugs, calcitonin, calcitriol and other bioactive
 CC steroids to intestinal, mucosal and lung epithelium. The method is also
 CC used for trans epithelial delivery of antigens to provoke tolerance and
 CC immunity. The method provides an immunisation, that specifically targets
 CC the mucosal surfaces, and does not have the risks associated with
 CC injections, including needle transmission of AIDS or hepatitis, of prior
 CC art immunisation methods. The present sequence represents the amino acid
 CC sequence of an Fc fragment of human immunoglobulin IgG.

Sequence 235 AA:
 Query Match 55.1%; Score 1237; DB 20; Length 235;
 Best Local Similarity 97.4%; Pred. No. 4, 1e-76;
 Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDKTHCPAPAPBELLGGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWY 60
 DB 2 vdkthcpapapbellggsvflfppkpkdtlmisrtpevtcvvdvshedpevkimwy 61
 QY 61 DGVEVHNAKTRPREOYNSTYRVASVLTALHODMLNGKVKCVSNKALPAPTEKTSKA 120
 DB 1 dgvevhnaktrpreoynstyrvasvltalhdwlngkvcvsnalpaplextlska 120

Db 62 gvevhnaktkpreegynstyrsvltvlnqdwlngkeyckvsnkalpajektlska 121
 QY 121 KGPREPQVYTLPPSRDELTKNOVSLTCLVGFYPSDIAVWESNGOPENNYKTTTPYLD 180
 Db 122 kgqprepvylppsrdeitknqvsitclvkgfypsdiavwesngqpenyktktppylid 181
 QY 181 SDGSFELYSKLTVDKSRWQGNVFSQSYMHEALNNHTQKSLSPGKETPPK 234
 Db 182 sdgsfilyskltvdksrwtgqgnviscsymhealnnhvtqkslslspgkxvtrpr 235

RESULT 5
 W26649
 ID W26649 standard; Protein; 651 AA.
 AC W26649;
 XX
 DT 12-FEB-1998 (first entry)
 Chimeric receptor hCTMO1/GI/zeta.

KW Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv;
 KW IgG1; T cell receptor zeta chain; cell proliferation; cytokine;
 KW inflammation; effector; cell differentiation; antibody secretion;
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft versus host disease; human; therapy.

XX Chimeric - Homo sapiens.
 XX
 PN W09723613-A2.
 PD 03-JUL-1997.
 XX
 PF 23-DEC-1996; 96MO-GB03209.
 XX
 PR 21-DEC-1995; 95GB-0026131.
 XX
 PA (CLLT) CELLTECH THERAPEUTICS LTD.
 XX
 PI Babbington CR, Flinney HM, Lawson ADG, Weir ANC;
 XX
 DR N-PSDB; T90512.
 XX
 XX New DNA systems for activating cells - comprising DNA coding for a
 P1 chimeric receptor comprising 2 or more different cytoplasmic
 XX signalling components.
 XX
 XX Disclosure; Fig 7; 90pp; English.

CC This protein comprises a chimeric receptor consisting of an scFv
 CC engineered from anti-CD3 human antibody CTMO1 linked to an
 CC extracellular spacer comprising the human IgG1 hinge, CH2 and CH3,
 CC linked to transmembrane and intracellular regions of the human T
 CC cell receptor zeta chain. It can be expressed in host cells (e.g.
 CC Jurkat) using a chimeric receptor gene (see T90512) constructed
 CC from DNA cassettes encoding each receptor component. In a claimed
 CC cell activation process an effector cell is transformed with DNA
 CC encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/idiopathic disease (claimed).

CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease, or diabetes (claimed).

SO Sequence 651 AA;
 Query Match 55.1%; Score 1236.5; DB 18; Length 651;
 Best Local Similarity 62.6%; Pred. No. 1.5e-75;
 Matches 258; Conservative 18; Mismatches 61; Indels 75; Gaps 9;

QY 2 DKHTCPPCAPPELUGSPVFLPPKPKDTLMSRPETVCVVVDVSHPEPKFKNYVD 61
 Db 288 dkhtcpccpapel199psvflfpkpkdtlmsrpetvcvvdvshpevkfnyvd 347
 QY 62 GVEVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAK 121
 Db 348 gvevhnaktkpreegynstyrsvltvlnqdwlngkeyckvsnkalpajektlska 407
 QY 122 GQPREPQVYTLPPSRDELTKNOVSLTCLVGFYPSDIAVWESNGOPENNYKTTTPYLD 181
 Db 408 gqprepvylppsrdeitknqvsitclvkgfypsdiavwesngqpenyktktppylid 467
 QY 182 DGSFELYSKLTVDKSRWQGNVFSQSYMHEALNNHTQKSLSPGKETPPKRYLHDEE 241
 Db 468 dgsfilyskltvdksrwtgqgnviscsymhealnnhvtqkslslspgkxvtrpr 518
 QY 242 TSHQLCDKCPPEGYTLKQHTAKKTKVCAPCPDHYTDSWHTDECLYCSYCKEQLYVK 301
 Db 519 tshqlcdkcppegytlkqhtakktkvcapcpdhytdswhtdecllycsyckeylvyk 540
 QY 302 -----QECNRHNRVCECKEGRYLEIFOLKHRSCPPGCVVQAGTPPERNTV 348
 Db 541 vkfarsadapayqggnqlynn--elnlgreeydvldkrrgrdpemg----gkprtr--- 590
 QY 349 CKRCPDGFSENETSKRKPCKRHNCVFGLLTQKNATHDNVCSCNSESTQ 400
 Db 591 -knpeegly-nelqkdkmaeyseigmkgerrrgkx--hdgilygslstck 637

RESULT 6
 W26650
 ID W26650 standard; Protein; 692 AA.
 AC W26650;
 XX
 DT 12-FEB-1998 (first entry)
 Chimeric receptor hCTMO1/GI/zeta-CD28.

KW Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv;
 KW IgG1; CD28; T cell receptor zeta chain; proliferation; cytokine;
 KW inflammation; effector; cell differentiation; antibody secretion;
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft versus host disease; human; therapy.

XX Chimeric - Homo sapiens.
 XX
 PN W09723613-A2.
 PD 03-JUL-1997.
 XX
 PF 23-DEC-1996; 96MO-GB03209.
 XX
 PR 21-DEC-1995; 95GB-0026131.
 XX
 PA (CLLT) CELLTECH THERAPEUTICS LTD.
 XX

PI Bebbington CR, Flinney HM, Lawson ADG, Weir ANC;
 XX WPI: 1997-351052/32.
 DR N-PSDB: T90513.
 XX
 PT New DNA systems for activating cells - comprising DNA coding for a
 PT chimeric receptor comprising 2 or more different cytoplasmic
 PT signalling components.
 PS
 PS Disclosure: Fig 8; 90pp; English.
 XX
 CC This protein comprises a chimeric receptor consisting of an scfv
 CC engineered from anti-CD3 human antibody C7MO1 linked to an
 CC extracellular spacer comprising the Human IgG1 hinge, CH2 and CH3,
 CC linked to the transmembrane and intracellular components of the
 CC human T cell receptor zeta chain, fused to the intracellular region
 CC of human CD28. It can be expressed in host cells (e.g. Jurkat)
 CC using a chimeric receptor gene (see T90513) constructed from DNA
 CC cassettes encoding each component of the receptor. In a claimed
 CC cell activation process an effector cell is transformed with DNA
 CC encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/adipopathic disease (claimed).
 CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease or diabetes (claimed).
 CC
 XX Sequence 692 AA:
 SQ

Query Match 55.1%; Score 1236.5; DB 18; Length 692;
 Best Local Similarity 62.6%; Pred. No. 1.6e-75;
 Matches 258; Conservative 18; Mismatches 61; Indels 75; Gaps 9;

QY 2 DKTHTCPCPAPPELLGSPVFLFPKPKDTLMSRPEVTCVVVDSHEDPEVKFNMYVD 61
 DB |||||||
 DB 288 dkhtctcpapapellgspvflfpkpkdtlmsrpevcvvvdshedpevkfnmyvd 347
 DB |||||||
 DB 62 GVEYHNAKTPREQYVSTRVSVTLVHODVLNGEKYCKVSKNKLPAPIETISKAK 121
 DB |||||||
 DB 348 gvevhnaktpreeqvstrvsvtlvlnqdwlngkyckvsknklpapietliskak 407
 DB |||||||
 QY 122 GOREPOVYTLPSRDELTKNOVSLTCLVKGFPYSDAVEMESGQENNYKTPPYLDS 181
 DB |||||||
 DB 408 gqreppvytlpsreemtknqvslclvngfypsdlavewesgqepennyktlppvids 467
 DB |||||||
 QY 182 DGSFFLYSKLTVDKSRMQQNVSCSVYHBAHNNHTQKSLSPGKETPPKYLHDEE 241
 DB |||||||
 DB 468 dgsfflyskltvdksrvgqnvscsvymhbalhnnhtqkslspgkettppkylhdee 518
 DB |||||||
 QY 242 TSHQOLCDKCPPTGYLKQCTAKKTYCACPDPHYTDSNHTSECLCYSPCKELOYVK 301
 DB |||||||
 DB 519 ----lc-----yldgllfylvlltalflr 540
 DB |||||||
 QY 302 -----QECNRTHNRCCECKRGRLIEFCLKHSRCPGPGVQAGTPERNTV 348
 DB |||||||
 DB 541 vkfsrsadapaygqgqqln---elnlgrteeydvldkrrgrdpemg-----gkprtr--- 590
 QY 349 CKRCPDGFSENETSSKAPCKRHTNCSVGLLLRQGNATHDNICSNSESTQ 400
 DB |||||||
 DB 591 -knpgegly-nelqkdkmaeayseigmgerirgk---hdglygstatk 637

RESULT 7
 R27163
 ID R27163 standard; Protein; 347 AA.
 XX
 AC R27163;
 XX
 DT 20-MAY-1998 (first entry)
 XX
 DE CD2 binding LFA-3-Ig fusion protein.
 XX
 KW Lymphocyte associated antigen-3; T-lymphocyte accessory molecule;
 KW deletion mutant; CD2 binding site; immunomodulator; immunoglobulin;
 KW preLFA3TIP; LFA-3(92)IgG; pSAB152; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT peptide 1..28
 FT /label= LFA-3-signal
 FT region 29..120
 FT /label= LFA-3.aminoacids_1-92
 FT region 121..130
 FT /label= IgG1_hinge
 FT domain 131..239
 FT /label= IgG1_CH2
 FT domain 240..347
 FT /label= IgG1_CH3
 XX
 PN EP503648-A.
 XX
 PD 16-SEP-1992.
 XX
 PF 12-MAR-1992: 92EP-0104320.
 XX
 PR 12-MAR-1991: 91US-0667971.
 PR 07-OCT-1991: 91US-0770967.
 XX
 PA (BIOI) BIOGEN INC.
 XX
 PI Miller GT, Rosa MD, Wallner BP;
 XX
 DR WPI: 1992-309760/38.
 DR N-PSDB: Q28684.
 XX
 XX CD2-binding domain of lymphocyte function associated antigen-3
 PT and DNA .. for diagnosing and treating inflammation and
 PT autoimmune diseases, e.g. systemic lupus erythematosus and
 PT rheumatoid arthritis
 PS
 PS Claim 13; Fig 12; 85pp; English.
 XX
 XX The plasmid pSAB152 contains the DNA sequence encoding the LFA-3
 CC signal sequence, the amino terminal 92 amino acids of mature LFA-3,
 CC ten amino acids of the hinge region of IgG1 and the CH2 and CH3
 CC constant domains of IgG1 (see Q28678-9 and Q28681-2 for details of
 CC the construction of pSAB152). A NotI fragment containing the coding
 CC sequence of pSAB152 was used in the construction of expression
 CC vector pMDR(92)Ig-3 which can be stably maintained in CHO cells to
 CC achieve continuous expression of LFA3TIP. The fusion protein can
 CC bind to CD2 and inhibit T cell activation, making it useful to
 CC treat acute and chronic inflammation, autoimmune disease and
 CC in immunomodulation.
 XX
 XX Sequence 347 AA:
 SQ

Query Match 54.9%; Score 1234; DB 13; Length 347;
 Best Local Similarity 99.68%; Pred. No. 1e-75;
 Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHNCPCPAPPELLGSPVFLFPKPKDTLMSRPEVTCVVVDSHEDPEVKFNMYVD 60
 |||||||

Db 120 vdkhtcpcpapellggsyflfpkpkdtlmistrpevtcvvvdshedpevkfmyv 179

OY 61 DGEVHNAKTRPREQYNSTRVSVLTVLHODWLNKEKCKVSNKALPAPIEKTISKA 120
 Db 180 dgevhnaaktpreeqynstyrvsvltvlhqdwlngkeyckvsnkalpapietkiska 239

OY 121 KGOPEPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 180
 Db 240 kgqprepqvylppsrdeltknqvslclvqfypsdlavewesngqpennyktcpvld 299

OY 181 SDGSFFLTKLTVDKSRMOQGNVFCSYMHEALHNHYTQKSLSLSPGK 228
 Db 300 sdgsfflyskltvdksrwtgqgnvfscsymhealhnhytqkslsispkg 347

RESULT 8
 ID Y83136 standard; Protein: 347 AA.
 Y83136:

DT 24-JUL-2000 (first entry)

DE Human transmembrane LFA-3/1gG fusion protein LFA3rip.

XX LFA3: CD2: cell signalling; modulation; lymphocyte; T cell;
 KW memory effector T lymphocyte; psoriatic arthritis;
 KW rheumatoid arthritis; multiple sclerosis; atopic dermatitis;
 KW uveitis; inflammatory bowel disease; Crohn's disease;
 KW ulcerative colitis; cutaneous T cell lymphoma; inhibition; treatment;
 KW therapy.

XX Homo sapiens.

OS WO200012113-A2.

PN 09-MAR-2000.

PD 31-AUG-1999; 99WO-US20026.

PF 31-AUG-1998; 98US-0098456.

PR (BIOJ) BIOGEN INC.

PA Magilav D;

PI WPI: 2000-282928/24.
 N-PSDB: 293401.

XX Selective modulation of memory effector T lymphocytes by administration
 PT of a CD2 binding agent which inhibits the CD2/LFA-3 interaction useful
 PT for treating conditions such as inflammatory bowel diseases, psoriatic
 PT arthritis

XX Disclosure; Page 75-76; 76pp; English.

PS Modulation of LFA3/CD2 interaction by administration of a CD2 binding
 CC agent inhibits CD2 signalling and T cell proliferation and activation
 CC and more particularly modulates the number and/or distribution of
 CC memory effector T lymphocytes. The method can be used for treating a
 CC condition in a subject where the condition is characterized by memory
 CC effector T lymphocytes playing a role in the pathogenesis of the
 CC condition such as psoriatic arthritis, rheumatoid arthritis,
 CC multiple sclerosis, atopic dermatitis, uveitis, inflammatory bowel
 CC disease, Crohn's disease, ulcerative colitis and cutaneous T cell
 CC lymphoma and where the method comprises administering to the subject
 CC an amount of CD2 binding agent sufficient to modulate the memory
 CC effector T lymphocytes. The methods provide inhibition of antigen
 CC specific interactions for all antigens present, inhibition of T cell
 CC activation, no general immunosuppression, and possibly induction of
 CC tolerance.

CC Sequence 347 AA:

Query Match 54.98; Score 1234; DB 21; Length 347;
 Best Local Similarity 99.68; Pred. No. 1e-73;
 Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKHHTCPCPAPELLGGSVFLFPKPKDTLMISRPPEVTCVVVDVSHEDPEVKFMYV 60
 Db 120 vdkhtcpcpapellggsyflfpkpkdtlmistrpevtcvvvdshedpevkfmyv 179

OY 61 DGEVHNAKTRPREQYNSTRVSVLTVLHODWLNKEKCKVSNKALPAPIEKTISKA 120
 Db 180 dgevhnaaktpreeqynstyrvsvltvlhqdwlngkeyckvsnkalpapietkiska 239

OY 121 KGOPEPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 180
 Db 240 kgqprepqvylppsrdeltknqvslclvqfypsdlavewesngqpennyktcpvld 299

OY 181 SDGSFFLTKLTVDKSRMOQGNVFCSYMHEALHNHYTQKSLSLSPGK 228
 Db 300 sdgsfflyskltvdksrwtgqgnvfscsymhealhnhytqkslsispkg 347

RESULT 9
 ID W73513 standard; Protein: 388 AA.
 W73513:

AC W73513;

DT 02-MAR-1999 (first entry)

DE Rabbit TGFbetaRII:Fc protein.

XX Transforming growth factor-beta receptor; TGF-beta receptor; arthritis;
 KW fusion protein; fibroproliferative disorder; diabetic nephropathy;
 KW glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis;
 KW collagen vascular disorder; therapy; rabbit.

XX Oryctolagus sp.

OS WO9848024-A1.

PN 29-OCT-1998.

PD 16-APR-1998; 98WO-US07587.

PF 18-APR-1997; 97US-0044641.

PR (BIOJ) BIOGEN INC.

PA Cate R, Gotwals P, Koteliarsky V, Sanicola-Nadel M;

PI WPI: 1998-609994/51.
 DR N-PSDB: V08998.

XX Transforming growth factor-beta receptor fusion protein - used to
 PT treat fibroproliferative disorders

XX Claim 4; Page 18-19; 70pp; English.

PS This sequence is a fusion protein of the rabbit transforming growth
 CC factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The
 CC encoded protein is an example of a protein of the invention, which are
 CC isolated TGF-beta receptor fusion proteins that competitively inhibit
 CC binding of TGF-beta to TGF-beta receptor. The fusion protein can be used
 CC in a method for lowering the levels of TGF-beta in an individual having
 CC arthritis. It can also be used to treat medical conditions such as
 CC fibroproliferative disorders. The fibroproliferative disorder is a
 CC kidney, intraocular or pulmonary fibrosis, especially selected from
 CC diabetic nephropathy, glomerulonephritis, proliferative
 CC vitreoretinopathy, or myelofibrosis. The fusion proteins can also be used
 CC to treat collagen vascular disorders, including systemic sclerosis,
 CC polymyositis, scleroderma, dermatomyositis, and systemic lupus

CC erythrematousus. They can also be administered following coronary
CC angioplasty, to prevent restenosis or scarring and reclosing of arteries
XX
50 Sequence 388 AA;

CC diabetic nephropathy, glomerulonephritis, proliferative
CC vitreoretinopathy, or myelofibrosis. The fusion proteins can also be used
CC to treat collagen vascular disorders, including systemic sclerosis,
CC polymyositis, scleroderma, dermatomyositis, and systemic lupus

| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 54.98; | Score 1234; | DB 19; | Length 388; |
| Best Local Similarity | 99.68; | Pred. NO. 1.2e-75; | | |
| Matches 227; | Conservative 1; | Mismatches 0; | Indels 0; | Gaps 0 |

Sequence 388 AA:

| | | | |
|----|-----|---|-----|
| Qy | 1 | MDKTTTCPCPCAPBELLGGSPVFLFPFKPKDKDLMSTRPEVLCVVAVDSDHEDPEVKFMVY | 60 |
| Db | 161 | vdktktcpcpcpapelllggsrvflfpbkpkcdtlmstrpevcvvavdshnepevkfmvy | 220 |
| Qy | 61 | DGEVHNAAKTRPREQVNSTRVSVLTVLVHODMLNGKEYKCYKSNKALPAPIEKTSTKA | 120 |
| Db | 221 | dgevhnaktkpreeqnustryvsvltvlvhdwlngkeykcvksnkalpap:ektlska | 280 |
| Qy | 121 | KGQRPQVYTLIPSRDELTKNQSILTCLVKGFIPSDIAVWESNGQRPENNYKTTTPVLD | 180 |
| Db | 281 | kgqrpqpyvtilpsrdelctknqysiltclvkgfipsdiavwesngqpenyktctpvld | 340 |
| Qy | 181 | SDGSFELYSKLTIVKSRMQGQNVFSCSVMHALLNNHYKQKLSLSPGK | 228 |
| Db | 341 | sdgsfelyskltlvksrwmqgnvfscsvmhailnhyqkqlslspspk | 388 |

| | | | | | | |
|----|---|--------|--------------------|--------|-------------|----------------------|
| | Query Match | 54.9% | Score 1234; | DB 19; | Length 388; | |
| | Best Local Similarity | 99.6%; | Pred. No. 1.2e-75; | | | |
| | Matches | 227; | Conservative | 1; | Mismatches | 0; Indels 0; Gaps 0; |
| OY | 1 MDKHTTCCPAPELLGGPSVFLFPPKKRDTLMISRTPEVTCVVVDVSHEDYEAKFNMTV | | | | | 60 |
| Db | : ktttctpcppcpelllqgspvflfpfkpkdtlmisrtpevtcvvdvsndepvknnwy | | | | | 220 |
| OY | 61 DGEVHNAAKTREEQYNSTRKWSVLTVLHODWLNKEEYKCKVSNNKALPAPIETISK | | | | | 120 |
| Db | 221 dgevhnaktkreeqynstryrsvslcvlbqdwlnkcykckvsnnkalpaplektiska | | | | | 280 |
| OY | 121 KGPREFQVYTLPRSRDELTKNQVSLTCLVKGFYSDSIAVEHESNGQPENNAIKTPPVLD | | | | | 180 |
| Db | 281 kgqrefqvylprsrdeltknqwsllclxkfypsdlavewesngqpennaiiktppvld | | | | | 340 |

| RESULT | 10 |
|--------|----------------------------------|
| W73514 | |
| ID | W73514 standard; Protein; 388 AA |

Db 341 sdgsfflyskltvdksrwgqgnvfscs

| | | |
|----|--------------------------------------|---------------|
| DT | 02-MAR-1999 | (first entry) |
| XX | | |
| DE | Human TGFbetarII:Fc protein sequence | |

| | | |
|----|---------|--------------------|
| ID | Y54063 | standard; Protein; |
| XX | | |
| AC | Y54063; | |

KM Transforming growth factor-beta receptor; TGF-beta receptor; arthritis
KM fusion protein; fibroproliferative disorder; diabetic nephropathy;
KM glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis;
KM collagen vascular disorder; therapy; human.

DT 27-MAR-2000 (first entry)
XX
XX Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion.
DE
XX

| | | |
|----|---------------|--------------|
| OS | Homo sapiens. | |
| XX | | |
| PN | W09848024-AL. | |
| XX | | |
| PD | 29-OCT-1998. | |
| XX | | |
| | | |
| | 16-APR-1998; | 98MO-US07587 |
| | | |
| | 18-APR-1997; | 97US-0044641 |

KM type II receptor; Fe portion; human IgG1; fusion protein; arthritis;
KM fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis;
KM diabetic nephropathy; glomerulonephritis; collagen vascular disease;
KM proliferative vitreoretinopathy; myelofibrosis; systemic sclerosis;
KM polymyositis; scleroderma; dermatomyositis; systemic lupus erythematosus;
KM restenosis; wound; connective tissue production; adhesion; scarring;
KM post-radiation fibrosis.
XX
XX
XX Synthetic.
XS

PI Cate R, Gotwals P, Korelliansky V, Sanicola-Nadcl M.
XX
DR WPI: 1998-609994/51.
DR N-PSDB: V08999.

| | |
|----|---------------|
| PN | WO9965948-A1. |
| XX | |
| PD | 23-DEC-1999. |
| XX | |

PT transforming growth factor-beta receptor fusion protein - used to
 PT treat fibroproliferative disorders
 XX
 PS Claim 4; Page 19-20; 70pp; English.

XX 16-JUN-1998; 9805-0089452.
PR
XX
PA (BIOJ) BIOGEN INC.

CC This sequence is a fusion protein of the human transforming growth
CC factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The
CC encoded protein is an example of a protein of the invention, which are +
CC isolated TGF-beta receptor fusion proteins that competitively inhibit
CC binding of TGF-beta to TGF-beta receptor. The fusion protein can be used
CC in a method for lowering the levels of TGF-beta in an individual having
CC arthritis. It can also be used to treat medical conditions such as
CC fibroproliferative disorders. The fibroproliferative disorder is a
CC kidney, intraocular or pulmonary fibrosis, especially selected from

PS Disclosure: Page 62-63; 69pp: English.
 CC The present sequence represents a splice variant of a rabbit transforming
 CC growth factor-beta (TGF-beta) type II receptor fused to the FC portion
 CC of human IgG1. The fusion protein has higher affinity for TGF-beta than
 CC fusion proteins comprising the non-variant form of the receptor. The
 CC fusion protein contains soluble TGF-beta receptor constructs that are
 CC devoid of a transmembrane region (and are secreted from the cell) but
 CC retain the ability to bind TGF-beta. The protein competitively inhibits
 CC binding of TGF-beta to cellular receptors and/or forms an inactive
 CC complex with TGF-beta. The protein is used to reduce levels of TGF-beta,
 CC for treatment of arthritic conditions associated with overexpression
 CC of TGF-beta, especially fibroproliferative diseases, e.g. renal,
 CC intra-ocular or pulmonary fibrosis; diabetic nephropathy;
 CC glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis;
 CC collagen vascular disease, e.g. systemic sclerosis; polymyositis;
 CC scleroderma, dermatomyositis or systemic lupus erythematosus; and
 CC fibrosis associated with restenosis. It is also used for treating
 CC wounds, to prevent overproduction of connective tissue and so prevent
 CC adhesions or scarring, and to prevent post-radiation fibrosis (by
 CC administration to patients about to undergo radiation therapy).

XX Sequence 388 AA;

Query Match 54.9%; Score 1234; DB 21; Length 388;
 Best Local Similarity 99.6%; Pred. No. 1.2e-75;
 Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPAPPELGGPSVFLFPPPKDMLISRTPEVTCVVDVSHEDPEVKFMVY 60
 Db 161 vdkthtcppapellggpsvflfpkpdkdmlstrpctvcvvdshedpevkfmvy 220
 QY 61 DGVVHNAAKTRPEQYNSTYRVSVLTVLAQDMLNGEKYCKVSNKALPAPIETKTSKA 120
 Db 221 dgyvhnaktkpreeqynstyrsvsltvlaqdwlngkeyckvsnkalpapietktska 280
 QY 121 KGQPREQVYTLPPSRDELTKNOVSLCLVKGFPSPDIAVEMSGNPENNYKTTTPVLD 180
 Db 281 kgqpreqvyltlppsrdeltkngvslclvkgfypsdiavewsnqpenmykttppvld 340
 QY 181 SDGSFLLSKLTVDKSRWQGNFSCSVMEHALNHYTKSLSPGK 228
 Db 341 sdgsfllskltvdksrwggnvfscsvmehalnhytqklsispkg 388

RESULT 12

Y54064 standard; Protein; 388 AA.

Y54064;

27-MAR-2000 (first entry)

Amino acid sequence for TGF-beta type II receptor variant/IgG1 fusion.

Splice variant: human; transforming growth factor-beta; TGF-beta;
 type II receptor; FC portion; human IgG1; fusion protein; arthritis;
 fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis;
 diabetic nephropathy; glomerulonephritis; collagen vascular disease;
 proliferative vitreoretinopathy; myelofibrosis; systemic sclerosis;
 polymyositis; scleroderma; dermatomyositis; systemic lupus erythematosus;
 restenosis; wound; connective tissue production; adhesion; scarring;
 post-radiation fibrosis.

XX Synthetic.
 XX Homo sapiens.
 XX WO965948-A1.
 XX 23-DEC-1999.
 XX 16-JUN-1999; 99MO-US13629.

XX 16-JUN-1998; 98US-0089452;
 XX (BIO) BIOGEN INC.
 XX Kotteliansky V., Gotwals P., Cate R., Sanicola-Nadel M;
 XX WPI; 2000-106083/09.
 XX N-PSDB; 245253, 245254.
 XX New fusion protein of a splice variant of transforming growth
 XX factor-beta receptor, for inhibiting the growth factor, e.g. in
 XX treatment of fibrosis

PS Disclosure: Page 64; 69pp: English.

CC The present sequence represents a splice variant of a human transforming
 CC growth factor-beta (TGF-beta) type II receptor fused to the FC portion
 CC of human IgG1. The fusion protein has higher affinity for TGF-beta than
 CC fusion proteins comprising the non-variant form of the receptor. The
 CC fusion protein contains soluble TGF-beta receptor constructs that are
 CC devoid of a transmembrane region (and are secreted from the cell) but
 CC retain the ability to bind TGF-beta. The protein competitively inhibits
 CC binding of TGF-beta to cellular receptors and/or forms an inactive
 CC complex with TGF-beta. The protein is used to reduce levels of TGF-beta,
 CC for treatment of arthritic conditions associated with overexpression
 CC of TGF-beta, especially fibroproliferative diseases, e.g. renal,
 CC intra-ocular or pulmonary fibrosis; diabetic nephropathy;
 CC glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis;
 CC collagen vascular disease, e.g. systemic sclerosis; polymyositis;
 CC scleroderma, dermatomyositis or systemic lupus erythematosus; and
 CC fibrosis associated with restenosis. It is also used for treating
 CC wounds, to prevent overproduction of connective tissue and so prevent
 CC adhesions or scarring, and to prevent post-radiation fibrosis (by
 CC administration to patients about to undergo radiation therapy).

XX Sequence. 388 AA;

Query Match 54.9%; Score 1234; DB 21; Length 388;
 Best Local Similarity 99.6%; Pred. No. 1.2e-75;
 Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPAPPELGGPSVFLFPPPKDMLISRTPEVTCVVDVSHEDPEVKFMVY 60
 Db 161 vdkthtcppapellggpsvflfpkpdkdmlstrpctvcvvdshedpevkfmvy 220
 QY 61 DGVVHNAAKTRPEQYNSTYRVSVLTVLAQDMLNGEKYCKVSNKALPAPIETKTSKA 120
 Db 221 dgyvhnaktkpreeqynstyrsvsltvlaqdwlngkeyckvsnkalpapietktska 280
 QY 121 KGQPREQVYTLPPSRDELTKNOVSLCLVKGFPSPDIAVEMSGNPENNYKTTTPVLD 180
 Db 281 kgqpreqvyltlppsrdeltkngvslclvkgfypsdiavewsnqpenmykttppvld 340
 QY 181 SDGSFLLSKLTVDKSRWQGNFSCSVMEHALNHYTKSLSPGK 228
 Db 341 sdgsfllskltvdksrwggnvfscsvmehalnhytqklsispkg 388

RESULT 13

Y70867 standard; Protein; 399 AA.

Y70867;

31-JUL-2000 (first entry)

Human interferon-beta-1a/mouse IgG2a FC fusion protein.

XX Human; interferon-beta-1a; IFN-beta-1a; immunoglobulin; fusion protein;
 KW angiogenesis; antisclerotic; antiinflammatory; immunosuppressive; cancer;
 KW cytostatic; virucide; hepatotropic; antiangiogenic; treatment; fibrosis;

KM multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis;
 KW viral infection; neovascularisation; mouse; IgG2a Fc domain.

OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.

FT Key Location/Qualifiers
 FT 1..166
 FT /label= natural_human_IFN-beta-1a
 FT 167..171
 FT /label= Enterokinase_linker
 FT 172..399
 FT Region /label= Mouse IgG2a-Fc portion
 FT /note= "comprises the hinge region, CH2 and CH3
 FT constant domains of mouse Ig"

XX WO200023472-A2.

XX 27-APR-2000.

XX 15-OCT-1999; 99WO-US24200.

XX 16-OCT-1998; 98US-0104491.

XX 16-FEB-1999; 99US-0120237.

XX (BIOI) BIOGEN INC.

XX Whitty A, Runkel L, Brickelmaier M, Hochman P;

XX WPI: 2000-339654/29.

XX N-PSDB; D00166.

XX Fusion proteins comprising interferon-beta-1a useful for inhibiting
 XX angiogenesis -

XX Example 2; Fig 2; 82pp; English.

XX The patent discloses fusion proteins comprising glycosylated
 CC interferon-beta (IFN-beta) especially an immunoglobulin (Ig) protein.
 CC non-IFN-beta proteins, especially an immunoglobulin (Ig) protein.
 CC The present sequence is a fusion protein that consists
 CC of mature human IFN-beta-1a and mouse IgG2a Fc domain separated by an
 CC enterokinase linker. The fusion protein is useful for
 CC inhibiting angiogenesis in a patient. It may also be used to treat
 CC multiple sclerosis, fibrosis, inflammatory and autoimmune diseases,
 CC cancers, hepatitis and viral infection characterised by
 CC neovascularisation.

XX Sequence 399 AA:

Query Match 54.9%; Score 1234; DB 21; Length 399;
 Best Local Similarity 99.6%; Pred. No. 1.2e-75;

Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKTHCCPCPAPRLGSPVFLPPKPKRTLMISRPEVTCVVDVSHDEPVKRWY 60

DB 172 vdkthccpapel19gspvflfppkpkclmistrpevcvvdshdepvkrmv 231

OY 61 DGEVHNATKPREEOYNSTRVAVSVLTVDHOMLNGKEKCKVSNKALPAPLEKITSKA 120

DB 232 dgevehnaktpreegynstrvavsvltvhdqwlngkeykckvsnkalpapektitska 291

OY 121 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPSDIAVWESNGQPENNYKTPPEVID 180

DB 292 kgqprepqvyltppsrde1tkngvsltc1vkgfypsdiavwesngqpennykttppvid 351

OY 181 SSGSFYLSKLTVDKSRMOGNFSSVMEALHNHYTQKSLSGCK 228

DB 352 ssgsfylskltvdksrmoqgnfssvmealhnhytqkslsispk 399

RESULT 14

Y70868
 ID Y70868 standard; Protein: 418 AA.

XX Y70868;

XX 31-JUL-2000 (first entry)

XX Human interferon-beta-1a G162C-IgG1 Fc direct fusion protein.

XX Human; interferon-beta-1a; IFN-beta-1a; immunoglobulin; fusion protein;

XX angiogenesis; antisclerotic; antiinflammatory; immunosuppressive; cancer;

XX cytostatic; virocid; hepatotropic; antiangiogenic; treatment; fibrosis;

XX multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis;

XX viral infection; neovascularisation; IgG1 Fc domain; VCAM-1; mutant;

XX vascular cell adhesion molecule-1.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..24

XX /label= VCAM-1-signal-sequence

XX /note= "Vascular cell adhesion molecule-1"

XX Protein 25..190

XX /label= natural_human_IFN-beta-1a

XX Misc-difference 186

XX /note= "Wild type IFN-beta-1a gly at position 162 is

XX substituted by Cys"

XX Region 192..418

XX /label= Human_IgG1-Fc-portion

XX /note= "comprises hinge, CH2 and CH3 domains of

XX IgG1 heavy chain"

XX WO200023472-A2.

XX 27-APR-2000.

XX 15-OCT-1999; 99WO-US24200.

XX 16-OCT-1998; 98US-0104491.

XX 16-FEB-1999; 99US-0120237.

XX (BIOI) BIOGEN INC.

XX Whitty A, Runkel L, Brickelmaier M, Hochman P;

XX WPI: 2000-339654/29.

XX N-PSDB; D00167.

XX Fusion proteins comprising interferon-beta-1a useful for inhibiting
 XX angiogenesis -

XX Example 5; Fig 10; 82pp; English.

XX The patent discloses fusion proteins comprising glycosylated

XX interferon-beta (IFN-beta) especially an immunoglobulin (Ig) protein.

XX non-IFN-beta proteins, especially an immunoglobulin (Ig) protein.

XX The present sequence is a fusion protein consisting of a vascular

XX cell adhesion molecule-1 (VCAM-1) signal sequence, a modified human

XX IFN-beta-1a and human IgG1 Fc domain, which are directly fused without

XX a linker sequence. The fusion protein is useful for

XX inhibiting angiogenesis in a patient. It may also be used to treat

XX multiple sclerosis, fibrosis, inflammatory and autoimmune diseases,

XX cancers, hepatitis and viral infection characterised by

XX neovascularisation.

XX Sequence 418 AA:

Query Match 54.9%; Score 1234; DB 21; Length 418;
 Best Local Similarity 99.6%; Pred. No. 1.3e-75;

Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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